

GenCore version 5.1.6  
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! protein - protein search, using sw model

on on: June 16, 2004, 13:24:56 ; Search time 59 Seconds  
(without alignments)  
2040.089 Million cell updates/sec

tie: US-09-095-478A-5

fect score: 426  
quence: 1 MSSPKVRGKTGRDNDEEG.....QYQFCYEIVLEVLQNLALY 426

oring table: OLIGO

Gapop 60.0 , Gapext 60.0

arched: 1586107 seqs, 282547505 residues

rd size : 0

al number of hits satisfying chosen parameters: 1586107

imum DB seq length: 0

ximum DB seq length: 2000000000

st-processing: Listing first 45 summaries

itabase : A\_Geneseq\_29Jan04.\*

1: geneseqp1980s.\*

2: geneseqp1990s.\*

3: geneseqp2000s.\*

4: geneseqp2001s.\*

5: geneseqp2002s.\*

6: geneseqp2003as.\*

7: geneseqp2003bs.\*

8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	426	100.0	426	2	AAW89249
2	405	95.1	405	2	AAW89251
3	383	89.9	463	2	AAW89250
4	29	6.8	29	2	AAW89264
5	29	6.8	29	2	AAW89263
6	29	6.8	29	2	AAW89265
7	23	5.4	122	2	AAW89252
8	19	4.5	261	6	AAE37994
9	19	4.5	398	5	ABG30845
10	19	4.5	398	7	ADD89795
11	19	4.5	409	7	ADQ09123
12	19	4.5	412	6	AAE37996
13	19	4.5	420	5	AAE14454
14	19	4.5	508	7	ADE08106
15	19	4.5	561	4	ABG06042
16	15	3.5	272	2	AAW67441
17	15	3.5	272	2	AAW34161
18	15	3.5	1105	4	AAW25567
19	15	3.5	1174	2	AAW67438
20	15	3.5	1174	2	AAW34158
21	15	3.5	1174	7	ADP45494
22	15	3.5	1175	7	ADP45494
23	15	3.5	1175	7	ADP45494
24	15	3.5	1175	7	ADP45494
25	14	3.3	176	2	AAW60876

26	14	3.3	245	4	AAW59389	AAW59389 Human pro
27	14	3.3	294	4	AAW78287	AAW78287 Human BCA
28	14	3.3	322	2	AAW60877	AAW60877 Product o
29	14	3.3	442	3	AAW56372	AAW56372 Human pro
30	14	3.3	607	3	AAW81783	AAW81783 Human pro
31	14	3.3	607	3	AAW56098	AAW56098 LAR tyros
32	14	3.3	647	4	AAW23746	AAW23746 Human EST
33	14	3.3	647	4	AAW14379	AAW14379 Human nov
34	14	3.3	1291	2	AAW75201	AAW75201 Tyrosine
35	14	3.3	1495	5	ABW57380	ABW57380 Rat mucoc
36	14	3.3	1496	7	ADW57115	ADW57115 Rat Prote
37	14	3.3	1496	7	ADW57119	ADW57119 Rat Prote
38	14	3.3	1496	7	ADD47013	ADD47013 Rat Prote
39	14	3.3	1496	7	ADD47017	ADD47017 Rat Prote
40	14	3.3	1501	2	AAW72858	AAW72858 Rat recep
41	14	3.3	1796	6	AAE37971	AAE37971 Human kin
42	14	3.3	1863	7	ADD46989	ADD46989 Rat Prote
43	14	3.3	1897	3	AAW81785	AAW81785 Human pro
44	14	3.3	1897	3	AAW56100	AAW56100 LAR tyros
45	14	3.3	1897	3	AAW19712	AAW19712 Human pro

## ALIGNMENTS

### RESULT 1

AAW89249 ID AAW89249 standard; protein; 426 AA.

XX AC

XX AAW89249;

DF 10-MAR-1999 (first entry)

DE Mouse PTP05.

XX XX

KW PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;

KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;

KW neurodegenerative disease; neuronal survival; Alzheimer's disease;

KW Parkinson's disease; Huntington's disease.

XX XX

OS Mus sp.

XX WO9849317-A2.

XX XX

PD 05-NOV-1998.

XX 27-APR-1998; 98WO-US008439.

XX 28-APR-1997; 97US-0044428P.

PR 20-MAY-1997; 97US-0047222P.

PR 11-JUN-1997; 97US-0049477P.

PR 11-JUN-1997; 97US-0049756P.

PR 18-JUN-1997; 97US-0049914P.

PR 23-OCT-1997; 97US-0063595P.

XX (SUGS-) SUGEN INC.

PA Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;

PI Courtneidge SA, App H, Hui TH;

XX WPI; 1999-009434/01.

DR N-PSDB; AAW81744.

XX New nucleic acid encoding specific protein tyrosine phosphatases - useful

XX for identifying specific modulators for treatment and prevention of

XX cancer and neurodegenerative disease.

XX Claim 2; Page 155-157; 193pp; English.

XX The present invention describes isolated, enriched or purified nucleic

XX acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The

XX present sequence represents mouse PTP05. The above proteins, other than

XX ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify

substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins

Sequence 426 AA;

Query Match 100.0%; Score 426; DB 2; Length 426;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MSSPRKVRGKTGRNDEEGSGNLNLSLPSSSQMTPTKPIFGNKNSENVPKSHHL 60  
 b 1 MSSPRKVRGKTGRNDEEGSGNLNLSLPSSSQMTPTKPIFGNKNSENVPKSHHL 60

Y 61 SPSDKYELVYPEPLESDTETVWDVDSRLNRNWSMDSETAGPSKTVSPVLSGSRLSK 120  
 b 61 SPSDKYELVYPEPLESDTETVWDVDSRLNRNWSMDSETAGPSKTVSPVLSGSRLSK 120

Y 121 DTETSVSEKELTQLAQIRPLIFNSSASAMRDCLNTLQKKEELDIREFLEQMTLPDD 180  
 b 121 DTETSVSEKELTQLAQIRPLIFNSSASAMRDCLNTLQKKEELDIREFLEQMTLPDD 180

Y 181 FNSGNTLQNRDKNRYDILPYDSTRVPLGKNKYINASYIRIWNHEEYFYIATQGPLPE 240  
 b 181 FNSGNTLQNRDKNRYDILPYDSTRVPLGKNKYINASYIRIWNHEEYFYIATQGPLPE 240

Y 241 TIEDFWQVLENNCNVIAITREIECGVICKYISWPISLKEPLEFEPHFVLETFHTVQY 300  
 b 241 TIEDFWQVLENNCNVIAITREIECGVICKYISWPISLKEPLEFEPHFVLETFHTVQY 300

Y 301 FTVRVFOIVKSKTGKSCQVXHLQFTKWPDHGTASADFFIKYVYVRKSHITGPLLPHCS 360  
 b 301 FTVRVFOIVKSKTGKSCQVXHLQFTKWPDHGTASADFFIKYVYVRKSHITGPLLPHCS 360

Y 361 AGVGTGVFICVDVVFSAIEKNYSFDIMNIVTQWRKORCGMIQTK 405  
 b 361 AGVGTGVFICVDVVFSAIEKNYSFDIMNIVTQWRKORCGMIQTK 405

# RESULT 2

AW89251

D AW89251 standard; protein; 405 AA.

C AW89251;

T 10-MAR-1999 (first entry)

E Mouse PTP05 isoform #2.

W PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;

N type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;

X neurodegenerative disease; neuronal survival; Alzheimer's disease;

X Parkinson's disease; Huntington's disease.

X Mus sp.

X WO9849317-A2.

X 05-NOV-1998.

X

X

X

X

X

X

X

X

X

X

X

X

X

X

X

PF 27-APR-1998; 98WO-US008439.

XX 28-APR-1997; 97US-0044428P.

ER 20-MAY-1997; 97US-0047222P.

PR 11-JUN-1997; 97US-0049477P.

PR 11-JUN-1997; 97US-0049756P.

PR 18-JUN-1997; 97US-0049914P.

PR 23-OCT-1997; 97US-0063595P.

XX (SUGB-) SUGEN INC.

XX Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;

PI Courtneidge SA, App H, Hui TH;

XX N-PSDB; AAV81746.

DR WPI; 1999-009434/01.

XX New nucleic acid encoding specific protein tyrosine phosphatases - useful

PT for identifying specific modulators for treatment and prevention of

PT cancer and neurodegenerative disease.

XX Claim 2; Page 158-160; 193pp; English.

XX The present invention describes isolated, enriched or purified nucleic

CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The

CC present sequence represents mouse PTP05. The above proteins, other than

CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify

CC substances that modulate their activity (i.e. agonists and antagonists,

CC including NBP) in vivo or in vitro. These substances are used to treat or

CC prevent diseases associated with abnormal signal transduction pathways

CC that involve the proteins, particularly cancer (e.g. leukaemia and

CC lymphoma), while modulators of ALK-7 (which is a type I receptor

CC serine/threonine kinase) are used to promote neuronal survival,

CC particularly for treating Alzheimer's, Parkinson's or Huntington's

CC diseases. Nucleic acid fragments of the polynucleotides encoding the

CC proteins can be used as probes to identify and clone related sequences;

CC to detect protein-encoded RNA; to generate transgenic animals and in gene

CC therapy (optionally after mutation). Ab are used to determine the

CC proteins

XX Sequence 405 AA;

XX Query Match 95.1%; Score 405; DB 2; Length 405;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSPRKVRGKTGRNDEEGSGNLNLSLPSSSQMTPTKPIFGNKNSENVPKSHHL 60

Db 1 MSSPRKVRGKTGRNDEEGSGNLNLSLPSSSQMTPTKPIFGNKNSENVPKSHHL 60

QY 61 SPSDKYELVYPEPLESDTETVWDVDSRLNRNWSMDSETAGPSKTVSPVLSGSRLSK 120

Db 61 SPSDKYELVYPEPLESDTETVWDVDSRLNRNWSMDSETAGPSKTVSPVLSGSRLSK 120

QY 121 DTETSVSEKELTQLAQIRPLIFNSSASAMRDCLNTLQKKEELDIREFLEQMTLPDD 180

Db 121 DTETSVSEKELTQLAQIRPLIFNSSASAMRDCLNTLQKKEELDIREFLEQMTLPDD 180

QY 181 FNSGNTLQNRDKNRYDILPYDSTRVPLGKNKYINASYIRIWNHEEYFYIATQGPLPE 240

Db 181 FNSGNTLQNRDKNRYDILPYDSTRVPLGKNKYINASYIRIWNHEEYFYIATQGPLPE 240

QY 241 TIEDFWQVLENNCNVIAITREIECGVICKYISWPISLKEPLEFEPHFVLETFHTVQY 300

Db 241 TIEDFWQVLENNCNVIAITREIECGVICKYISWPISLKEPLEFEPHFVLETFHTVQY 300

QY 301 FTVRVFOIVKSKTGKSCQVXHLQFTKWPDHGTASADFFIKYVYVRKSHITGPLLPHCS 360

Db 301 FTVRVFOIVKSKTGKSCQVXHLQFTKWPDHGTASADFFIKYVYVRKSHITGPLLPHCS 360

QY 361 AGVGTGVFICVDVVFSAIEKNYSFDIMNIVTQWRKORCGMIQTK 405

Db 361 AGVGTGVFICVDVVFSAIEKNYSFDIMNIVTQWRKORCGMIQTK 405

## SULT 3

M89250

AAW89250 standard; protein; 463 AA.

AAW89250;

10-MAR-1999 (first entry)

Mouse PTP05 isoform #1.

PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease.

Mus sp.

WO9849317-A2.

05-NOV-1998.

27-APR-1998; 98WO-US008439.

28-APR-1997; 97US-0044428P.

20-MAY-1997; 97US-0047222P.

11-JUN-1997; 97US-0049477P.

11-JUN-1997; 97US-0049756P.

18-JUN-1997; 97US-0049914P.

23-OCT-1997; 97US-0063595P.

(SUG2-) SUGEN INC.

Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D; Courtneidge SA, App H, Rui TH;

WPI; 1999-009434/01.

N-PSDB; AAV81745.

New nucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.

Claim 2; Page 157-158; 193pp; English.

The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence represents mouse PTP05. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins

Sequence 463 AA;

Query Match 89.9%; Score 383; DB 2; Length 463;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

44 IFGNKXNSNVKPSHLSFSDXYELVPEPLESDTETVWDSRSLNRNWSXDSAG 103

|||||

81 IFGNKXNSNVKPSHLSFSDXYELVPEPLESDTETVWDSRSLNRNWSXDSAG 140

|||||

QY 104 PSKTVSPVLSSGSRSLSKDTSTVSSEKELTOLAQIRPLIFNSSARSAMRDCINTLOKKEEL 163  
 DB |||||  
 141 PSKTVSPVLSSGSRSLSKDTSTVSSEKELTOLAQIRPLIFNSSARSAMRDCINTLOKKEEL 200  
 QY 164 DIREFLELEOMTLPPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIV 223  
 DB |||||  
 201 DIREFLELEOMTLPPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIV 260  
 QY 224 NHEBEYFYIATQGPLPETIEDFWQVLENNCNVIMITREIEGCVIKCYSWPIISKEPL 283  
 DB |||||  
 261 NHEBEYFYIATQGPLPETIEDFWQVLENNCNVIMITREIEGCVIKCYSWPIISKEPL 320  
 QY 284 ETEHFSVLETFHTVTOYETVRVQIVKKSQKQVAKHLOFTKWPDRHGTTPASADFFIKYV 343  
 DB |||||  
 321 ETEHFSVLETFHTVTOYETVRVQIVKKSQKQVAKHLOFTKWPDRHGTTPASADFFIKYV 380  
 QY 344 RYVRKSHITGELLVHCSAGVGRITGVFICVDWFSATKKNYSFDMNIVTQMRKQRCQMIQ 403  
 DB |||||  
 381 RYVRKSHITGELLVHCSAGVGRITGVFICVDWFSATKKNYSFDMNIVTQMRKQRCQMIQ 440  
 QY 404 TKEQYQFCYEIVLEVLQNLALY 426  
 DB |||||  
 441 TKEQYQFCYEIVLEVLQNLALY 463

## RESULT 4

AAW89264

ID AAW89264 standard; peptide; 29 AA.

XX AC AAW89264;

XX DT 10-MAR-1999 (first entry)

XX DE Human PTP05 peptide 431A.

XX KW PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease.

OS Homo sapiens.

XX PN WO9849317-A2.

XX PD 05-NOV-1998.

XX PE 27-APR-1998; 98WO-US008439.

XX PR 28-APR-1997; 97US-0044428P.

XX PR 20-MAY-1997; 97US-0047222P.

XX PR 11-JUN-1997; 97US-0049477P.

XX PR 11-JUN-1997; 97US-0049756P.

XX PR 18-JUN-1997; 97US-0049914P.

XX PR 23-OCT-1997; 97US-0063595P.

XX (SUG2-) SUGEN INC.

XX PA Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;

XX PI Courtneidge SA, App H, Rui TH;

XX XX WPI; 1999-009434/01.

XX PT New nucleic acid encoding specific protein tyrosine phosphatases - useful

XX PT for identifying specific modulators for treatment and prevention of

XX PT cancer and neurodegenerative disease.

XX PS Example 14; Page 108; 193pp; English.

XX CC The present invention describes isolated, enriched or purified nucleic

XX CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The

XX CC above proteins, other than ALK-7, are protein tyrosine phosphatases

XX CC (PTPs) and are used to identify substances that modulate their activity

XX CC (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These

substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins. The present sequence represents a human PTP05 peptide from the present invention

Sequence 29 AA;

Query Match 6.8%; Score 29; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.3e-21;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 109 SPVLGSSRLSKDTTSVSEKELTQLAQI 137  
|||||  
1 SPVLGSSRLSKDTTSVSEKELTQLAQI 29

RESULT 5  
AAW89263  
D AAW89263 standard; peptide; 29 AA.

AAW89263;

1 10-MAR-1999 (first entry)

Human PTP05 peptide 433A.

PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;  
type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;  
neurodegenerative disease; neuronal survival; Alzheimer's disease;  
Parkinson's disease; Huntington's disease.

Homo sapiens.

WO9849317-A2.

05-NOV-1998.

27-APR-1998; 98WO-US008439.

28-APR-1997; 97US-0044428P.

20-MAY-1997; 97US-0047222P.

11-JUN-1997; 97US-0049477P.

11-JUN-1997; 97US-0049756P.

18-JUN-1997; 97US-0049914P.

23-OCT-1997; 97US-0063595P.

(SUGEN-) SUGEN INC.

Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;

Courtneidge SA, App H, Hui TH;

WPI; 1999-009434/01.

New nucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.

Example 14; Page 108; 193pp; English.

The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly

cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins. The present sequence represents a human PTP05 peptide from the present invention

Sequence 29 AA;

Query Match 6.8%; Score 29; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.3e-21;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSPRKVRGKTGRDNDDEEGNSGNLNLEN 29  
DB 1 MSSPRKVRGKTGRDNDDEEGNSGNLNLEN 29

RESULT 6

AAW89265  
ID AAW89265 standard; peptide; 29 AA.

AAW89265;

10-MAR-1999 (first entry)

Human PTP05 peptide 432A.

PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;  
type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;  
neurodegenerative disease; neuronal survival; Alzheimer's disease;  
Parkinson's disease; Huntington's disease.

Homo sapiens.

WO9849317-A2.

05-NOV-1998.

27-APR-1998; 98WO-US008439.

28-APR-1997; 97US-0044428P.

20-MAY-1997; 97US-0047222P.

11-JUN-1997; 97US-0049477P.

11-JUN-1997; 97US-0049756P.

18-JUN-1997; 97US-0049914P.

23-OCT-1997; 97US-0063595P.

(SUGEN-) SUGEN INC.

Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;

Courtneidge SA, App H, Hui TH;

WPI; 1999-009434/01.

New nucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.

Example 14; Page 108; 193pp; English.

The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal



survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins. The present sequence represents a human PTP05 peptide from the present invention

Sequence 29 AA;

Query Match 6.8%; Score 29; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.3e-21;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

83 WDVSDRLNRNWMDSGTAGPSKTVSPV 111  
|||||  
1 WDVSDRLNRNWMDSGTAGPSKTVSPV 29

RESULT 7  
AAW89252  
AAW89252 standard; protein; 122 AA.

AAW89252;

10-MAR-1999 (first entry)

Rat PTP10.

PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease.

Rattus sp.

WO9849317-A2.

05-NOV-1998.

27-APR-1998; 98WO-US008439.

28-APR-1997; 97US-0044428P.

20-MAY-1997; 97US-0047222P.

11-JUN-1997; 97US-0049477P.

11-JUN-1997; 97US-0049756P.

18-JUN-1997; 97US-0049914P.

23-OCT-1997; 97US-0063595P.

(SUGEN) SUGEN INC.

Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;

Courtneidge SA, App H, Hui TH;

WPI: 1999-009434/01.

N-PSDB; AA81747.

New nucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.

Claim 2; Page 160; 193pp; English.

The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence represents rat PTP10. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival.

CC particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins

Sequence 122 AA;

Query Match 5.4%; Score 23; DB 2; Length 122;  
Best Local Similarity 100.0%; Pred. No. 6.8e-15;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 DFFIKYVYVRKSHITGPLLVC 359

DB 94 DFFIKYVYVRKSHITGPLLVC 116

RESULT 8

AAE37994

ID AAE37994 standard; protein; 261 AA.

XX AAE37994;

XX 06-NOV-2003 (first entry)

DT Human kinase and phosphatase (KPP-39) protein.

DE Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis; atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer;

KW psoriasis; thrombocytopenia; developmental disorder; Reiter's syndrome; renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease; neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis; autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome; acquired immune deficiency syndrome; immunosuppressive; Crohn's disease; neutropenic; dermatitis; multiple sclerosis; diabetes mellitus; allergic; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome; osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological; gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.

XX Homo sapiens.

XX WO2003050084-A2.

XX 19-JUN-2003.

XX 06-DEC-2002; 2002WO-US039126.

XX 07-DEC-2003; 2001US-0340235P.

XX 19-DEC-2003; 2001US-0343007P.

XX 21-DEC-2003; 2001US-0343546P.

XX 04-FEB-2002; 2002US-0354388P.

XX 15-FEB-2002; 2002US-0357675P.

XX (INCY-) INCYTE GENOMICS INC.

XX Kable AE, Chien D, Wilson AD, Swarnakar A, Gorvad AE;

XX Kafalia AJA, Emerling BM, Runkumar J, Jin P, Griffin JA, Marquis JP;

XX Baughn MR, Chawla NK, Lehr-Mason PM, Khare R, Lee S, Hawkins PR;

XX Becha SD, Lee SY, Sprague WW, Zebarjadian Y;

XX WPI: 2003-532894/50.

XX N-PSDB; AAD57366.

XX New human kinases and phosphatases and polynucleotides, useful for

PT diagnosing, treating or preventing autoimmune or inflammatory disorders

PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,

PT cancer or hepatitis.

XX Claim 1; Page 242; 282pp; English.

XX The invention relates to an isolated polypeptide, which is a human kinase

CC and phosphatase (KPP). KPP agonists and antagonists are useful for

diagnosing, treating or preventing disorders associated with aberrant expression of KPP, particularly cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary thrombocytopaenia or cancer), developmental disorders (eg renal tubular acidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome, allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral, bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP is useful in assessing the effects of exogenous compounds on the expression of nucleic acids and kinases and phosphatases. KPP gene is useful in gene therapy and for creating transgenic animals to model human disease. The present sequence is human KPP protein

Sequence 261 AA;

Query Match 4.5%; Score 19; DB 6; Length 261;  
Best Local Similarity 100.0%; Pred. No. 1.7e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

192 KNYRDILPYDSTRVPLGK 210  
|||||  
27 KNYRDILPYDSTRVPLGK 45

RESULT 9  
XG30845  
ABG30845 standard; protein; 398 AA.

ABG30845;

21-OCT-2002 (first entry)

Human tyrosine phosphatase protein #1.

Human; tyrosine phosphatase; obesity; diabetes; Parkinson's disease;  
central nervous system disorder; CNS; cardiovascular disorder; stroke;  
chronic obstructive pulmonary disease; cancer; multiple sclerosis;  
Alzheimer's disease; Huntington's disease; congestive heart failure;  
myocardial infarction; chromosome 10.

Homo sapiens.

WO200242435-A2.

30-MAY-2002.

27-NOV-2001; 2001WO-EP013794.

27-NOV-2000; 2000US-0252912P.

(FARB ) BAYER AG.

Zhu Z;

WPI: 2002-575236/61.

N-PSDB; ABK89178.

New human tyrosine phosphatase polypeptide, the regulation of which is useful for treating obesity, diabetes, cardiovascular or central nervous system disorder, chronic obstructive pulmonary disease and cancer.

Claim 25; Fig 2; 145pp; English.

The present invention relates to a new human tyrosine phosphatase polypeptide. The invention is useful for the preparation of a medicament for modulating the activity of human tyrosine phosphatase in a disease such as obesity, diabetes, a central nervous system (CNS) disorder,

chronic obstructive pulmonary disease, cardiovascular disorder or cancer. The invention is useful for treating a human tyrosine phosphatase dysfunction related disease, preferably the above mentioned diseases. The invention is useful for treating the above mentioned disorders, where the CNS disorder is selected from Parkinson's disease, multiple sclerosis, stroke, Alzheimer's disease, and Huntington's disease, and the cardiovascular disorder is selected from congestive heart failure and myocardial infarction. The molecules of the invention are useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to disease and abnormalities related to the presence of mutations in the polynucleotide coding the polypeptide of the invention. The present amino acid sequence represents the human tyrosine phosphatase protein #1 of the invention. This sequence is encoded by the human tyrosine phosphatase gene located on chromosome 10

Sequence 398 AA;

Query Match 4.5%; Score 19; DB 5; Length 398;  
Best Local Similarity 100.0%; Pred. No. 2.6e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 KNYRDILPYDSTRVPLGK 210

Db 164 KNYRDILPYDSTRVPLGK 182

RESULT 10

ADD89795

ID ADD89795 standard; protein; 398 AA.

AC ADD89795;

XX 29-JAN-2004 (first entry)

XX Human DKF2P566K0524 protein SEQ ID NO:10.

XX cancer associated phosphatase; enzyme; human; cancer; tumour; cytostatic;  
XX immunosuppressive; antidiabetic; neuroprotective; antirheumatic;  
XX antiarthritic; antipsoriatic; antiarteriosclerotic; antiinflammatory;  
XX vulnery; gynaecological; angiogenic; hyperproliferative disease;  
XX autoimmune disease; diabetes mellitus; multiple sclerosis;  
XX rheumatoid arthritis; psoriasis; atherosclerosis; inflammation; scarring;  
XX endometriosis; angiogenesis.

OS Homo sapiens.

XX WO2003083102-A2.

XX 09-OCT-2003.

XX 19-MAR-2003; 2003WO-CA000393.

XX 28-MAR-2002; 2002US-0368859P.

XX (KINE-) KINETEK PHARM INC.

XX Delaney AD;

XX WPI: 2003-902934/82.

XX N-PSDB; ADD89794.

XX New nucleic acids encoding cancer associated phosphatases, useful as targets for screening pharmaceutical agents that inhibit the growth of tumor cells, or for diagnosing and treating cancer, inflammation or autoimmune disease.

XX Claim 1; SEQ ID NO 10; 63pp; English.

XX The present invention describes an isolated cancer associated phosphatase nucleic acid. Also described: (1) a method of screening for biologically active agents that modulate a cancer associated phosphatase function; (2) a method for the diagnosis of cancer; (3) a method for inhibiting the growth of a cancer cell; (4) methods of screening for targets of a cancer

associated phosphatase, where the targets are associated with signal transduction in cancer cells; (5) a compound (C) for the treatment of a tumour; (6) a composition for the treatment of a tumour comprising a pharmaceutical carrier and (C); (7) methods for treating a tumour; and (8) a method for visualising a tumour in a patient. A cancer associated phosphatase of the present invention has cytostatic, immunosuppressive, antidiabetic, neuroprotective, antirheumatic, antiarthritic, antipsoriatic, antiarteriosclerotic, antiinflammatory, vulnerary, gynaecological and antiangiogenic activities. The cancer associated phosphatases and nucleic acids encoding the proteins are useful for visualising tumours in patients or diagnosing and treating cancer, e.g. pancreas, lung, ovarian, liver or colon cancer. The polypeptides and nucleic acids may also be used for treating hyperproliferative diseases, such as autoimmune disease, diabetes mellitus, multiple sclerosis, rheumatoid arthritis, psoriasis, atherosclerosis, inflammation, scarring, endometriosis or angiogenesis, determining the effectiveness of drugs, determining patient prognosis, or as targets for screening pharmaceutical agents that inhibit the growth or metastasis of tumour cells. The present sequence represents the human cancer associated phosphatase DKF2P566K0524, which is used in the exemplification of the present invention.

Sequence 398 AA;

Query Match 4.5%; Score 19; DB 7; Length 398;  
Best Local Similarity 100.0%; Pred. No. 2.6e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

192 KNYRDILPYDSTRVPLCK 210  
|||||  
164 KNYRDILPYDSTRVPLCK 182

RESULT 11

AE09123  
ADE09123 standard; protein; 409 AA.

ADE09123;

29-JAN-2004 (first entry)

Novel protein-related contig polypeptide sequence #189.

novel gene; novel protein; tissue marker; molecular weight marker;  
chromosome marker; genetic disorder; contig.

Unidentified.

WO2003054152-A2.

03-JUL-2003.

10-DEC-2002; 2002WO-US039555.

10-DEC-2001; 2001US-0335739P.

11-DEC-2001; 2001US-033453P.

14-MAR-2002; 2002US-0365091P.

14-MAR-2002; 2002US-0365384P.

12-APR-2002; 2002US-0372381P.

12-APR-2002; 2002US-0372615P.

22-APR-2002; 2002US-00128558.

24-APR-2002; 2002US-0376045P.

(HYSE-) HYSEQ INC.

Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;  
Ma Y, Wang D, Chen R, Xu C, Boyle BJ;

WPI; 2003-569235/53.

New polynucleotides, useful for expressing recombinant proteins for  
analysis, characterization or therapeutic use, or as markers for tissues

PT in which the corresponding protein is preferentially expressed.

XX Disclosure; SEQ ID NO 2667; 1177pp; English.

XX The invention comprises the amino acid and coding sequences of novel  
XX proteins. The DNA and protein sequences of the invention are useful as:  
XX markers for tissues in which the corresponding protein is preferentially  
XX expressed; as molecular weight markers on gels; as chromosome markers or  
XX tags; to identify chromosomes or to map related gene positions; and to  
XX compare with endogenous DNA sequences in patients to identify potential  
XX genetic disorders. The present amino acid sequence was used in the  
XX exemplification of the invention.

XX Sequence 409 AA;

Query Match 4.5%; Score 19; DB 7; Length 409;

Best Local Similarity 100.0%; Pred. No. 2.6e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 KNYRDILPYDSTRVPLCK 210

DB 175 KNYRDILPYDSTRVPLCK 193

RESULT 12

AAE37996

ID AAE37996 standard; protein; 412 AA.

XX AAE37996;

DT 06-NOV-2003 (first entry)

XX Human kinase and phosphatase (KPP-41) protein.

XX Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis;  
XX atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer;  
XX psoriasis; thrombocytopenia; developmental disorder; Reiter's syndrome;  
XX renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease;  
XX neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis;  
XX autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome;  
XX acquired immune deficiency syndrome; immunosuppressive; Crohn's disease;  
XX neutropenic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus;  
XX allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome;  
XX osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological;  
XX gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.

XX Homo sapiens.

XX WO2003050084-A2.

XX 19-JUN-2003.

XX 06-DEC-2002; 2002WO-US039126.

XX 07-DEC-2001; 2001US-0340235P.

XX 19-DEC-2001; 2001US-0343007P.

XX 21-DEC-2001; 2001US-0343546P.

XX 04-FEB-2002; 2002US-0354388P.

XX 15-FEB-2002; 2002US-0357675P.

XX (INCY-) INCYTE GENOMICS INC.

XX Kable AB, Chien D, Wilson AD, Swarnakar A, Gorvad AE;

XX Hafalia AJA, Emerling BM, Ramkumar J, Jin P, Griffin JA, Marquis JP;

XX Baugun MR, Chawla NK, Lehr-Mason PM, Khare R, Lee S, Hawkins PR;

XX Becha SD, Lee SY, Sprague WW, Zebarjadian Y;

XX WPI; 2003-532894/50.

XX N-PSDB; AAD57368.

XX New human kinases and phosphatases and polynucleotides, useful for  
XX diagnosing, treating or preventing autoimmune or inflammatory disorders  
XX (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,

cancer or hepatitis.

Claim 1; Page 243-244; 282pp; English.

The invention relates to an isolated polypeptide, which is a human kinase and phosphatase (KPP). KPP agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of KPP, particularly cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary thrombocytopaenia or cancer), developmental disorders (eg. renal tubular acidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome, allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral, bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP is useful in assessing the effects of exogenous compounds on the expression of nucleic acids and kinases and phosphatases. KPP gene is useful in gene therapy and for creating transgenic animals to model human disease. The present sequence is human KPP protein

Sequence 412 AA;

Query Match 4.5%; Score 19; DB 6; Length 412;  
Best Local Similarity 100.0%; Pred. No. 2.6e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

192 KNYRDILFYDSTRVPLGK 210  
186 KNYRDILFYDSTRVPLGK 204

35214454  
AAE14454 standard; protein; 420 AA.

AAE14454;

26-MAR-2002 (first entry)

Human protein phosphatase-4.

Human; protein phosphatase; PP-4; immune system disorder; AIDS; allergy; neurological disorder; developmental disorder; Alzheimer's disease; cell proliferative disorder; Huntington's disease; arteriosclerosis; renal tubular acidosis; gonadal dysgenesis; cancer; adenocarcinoma; leukaemia; transgenic animal; gene therapy.

Homo sapiens.

Key Location/Qualifiers  
Region 183..411  
/note="Protein-tyrosine phosphatase"  
Active-site 340..388  
/note="Tyrosine specific protein phosphatase active site"  
Region 351..363  
/note="Tyr\_phosphatase"  
Domain 362..379  
/label="Transmembrane\_domain"

WO2001196546-A2.

20-DEC-2001.

14-JUN-2001; 2001WO-US019442.

16-JUN-2000; 2000US-0212447P.  
22-JUN-2000; 2000US-0213746P.

29-JUN-2000; 2000US-0215210P.  
06-JUL-2000; 2000US-0216529P.  
12-JUL-2000; 2000US-0218080P.  
21-JUL-2000; 2000US-0220117P.

(INCY-) INCYTE GENOMICS INC.

Au-Young J, Baughn MR, Ding L, Elliott VS, Gandhi AR, Griffin JA; Hafalia A, Kearney L, Lee EA, Lu Y, Nguyen DB, Patterson C; Ramkumar J, Reddy R, Sanjanwala MS, Stewart EA, Tang YT, Thornton M; Tribouley CM, Walia NK, Yang J, Yao MG, Yue H;

WPI: 2002-090206/12.  
N-PDB; AAD24022.

Novel polypeptide, useful for diagnosing, treating or preventing disorders of growth and development, immune system, neurological and cell proliferation diseases, comprises cancer protein phosphatase polypeptides.

Claim 1; Page 105-106; 116pp; English.

The present sequence is human protein phosphatase (PP)-4. PP polynucleotide and polypeptide are useful in the diagnosis, treatment and prevention of immune system disorders, neurological disorders, developmental disorders and cell proliferative disorders. Examples of immune system disorders include acquired immune deficiency syndrome (AIDS), severe combined immunodeficiency disease (SCID), adult respiratory distress syndrome, allergies, amyloidosis, anaemia, asthma, atherosclerosis, Crohn's disease, atopic dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout, Graves' disease, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, rheumatoid arthritis, Sjogren's syndrome, scleroderma, systemic osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome, sclerositis, trauma; neurological disorders include Alzheimer's disease, Huntington's disease, dementia, epilepsy, Parkinson's disease, mental retardation and other developmental disorders of central nervous system such as Down's syndrome, cerebral palsy, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder such as akathisia, amnesia, catatonia, dyskinesia; developmental disorders include e.g. renal tubular acidosis, Duchenne and Becker muscular dystrophy, gonadal dysgenesis, hypothyroidism; cell proliferative disorders include e.g. actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, psoriasis and cancer including adenocarcinoma, leukaemia. The polypeptide and polynucleotide are further useful for analysing proteome of a tissue or a cell type, for screening an agonist/antagonist, a compound that specifically binds to it or its modulator. The polynucleotide is useful for creating knockin humanised animals (pigs) or transgenic animals (mice or rats) to model human disease, for generating a transcript image of a tissue or cell type, which represents the global pattern of gene expression by a particular tissue or cell type

Sequence 420 AA;

Query Match 4.5%; Score 19; DB 5; Length 420;  
Best Local Similarity 100.0%; Pred. No. 2.7e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

192 KNYRDILFYDSTRVPLGK 210  
186 KNYRDILFYDSTRVPLGK 204

RESULT 14  
ADE08106  
ID ADE08106 standard; protein; 508 AA.  
XX  
AC ADE08106;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Novel protein (useful for identifying genetic disorders) #261.

novel gene; novel protein; tissue marker; molecular weight marker;  
chromosome marker; genetic disorder.

Unidentified.

WO2003054152-A2.

03-JUL-2003.

10-DEC-2002; 2002WO-US039555.

10-DEC-2001; 2001US-0339739P.

11-DEC-2001; 2001US-0339453P.

14-MAR-2002; 2002US-0365093P.

14-MAR-2002; 2002US-0365384P.

12-APR-2002; 2002US-0372381P.

12-APR-2002; 2002US-0372615P.

22-APR-2002; 2002US-00128558.

24-APR-2002; 2002US-0376045P.

(HYSE-) HYSEQ INC.

Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;

Ghoah M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;

Ma Y, Wang D, Chen R, Xu C, Boyle B;

WPI; 2003-569235/53.

N-PSDB; ADE07195.

New polynucleotides, useful for expressing recombinant proteins for  
analysis, characterization or therapeutic use, or as markers for tissues  
in which the corresponding protein is preferentially expressed.

Claim 20; SEQ ID NO 1172; 1177pp; English.

The invention comprises the amino acid and coding sequences of novel  
proteins. The DNA and protein sequences of the invention are useful as:  
markers for tissues in which the corresponding protein is preferentially  
expressed; as molecular weight markers on gels; as chromosome markers or  
tags; to identify chromosomes or to map related gene positions; and to  
compare with endogenous DNA sequences in patients to identify potential  
genetic disorders. The present amino acid sequence represents a protein  
of the invention.

Sequence 508 AA;

Query Match 4.5%; Score 19; DB 7; Length 508;

Best Local Similarity 100.0%; Pred. No. 3.2e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

192 KNYRDILPYDSTRVPLGK 210

|||||

274 KNYRDILPYDSTRVPLGK 292

SULT 15

ABG06042

ABG06042 standard; protein; 561 AA.

ABG06042;

13-FEB-2002 (first entry)

Novel human diagnostic protein #6033.

Human; chromosome mapping; gene mapping; gene therapy; forensic;  
food supplement; medical imaging; diagnostic; genetic disorder.

Homo sapiens.

WO200175067-A2.

PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AAS70229.

XX New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

XX biodiversity.

PS Claim 20; SEQ ID NO 36401; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic

CC amino acid sequences of the invention. Note: The sequence data for this

CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 561 AA;

Query Match 4.5%; Score 19; DB 4; Length 561;

Best Local Similarity 100.0%; Pred. No. 3.5e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 KNYRDILPYDSTRVPLGK 210

|||||

Db 327 KNYRDILPYDSTRVPLGK 345

Search completed: June 16, 2004, 13:31:29

Job time : 60 secs

GenCore version 5.1.6  
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protein - protein search, using sw model

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(without alignments)  
956.203 Million cell updates/sec

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Index score: 426  
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- 3: /cgm2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgm2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgm2\_6/ptodata/2/iaa/PCRTUS\_COMB.pep.\*
- 6: /cgm2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	3.5	272	US-08-446-345-34	Sequence 34, Appl
2	15	3.5	1174	US-08-446-345-36	Sequence 36, Appl
3	14	3.3	176	US-08-036-210-9	Sequence 9, Appl
4	14	3.3	176	US-08-449-609-9	Sequence 9, Appl
5	14	3.3	176	US-09-361-096A-9	Sequence 9, Appl
6	14	3.3	245	US-08-685-992-26	Sequence 26, Appl
7	14	3.3	245	US-09-144-925-26	Sequence 26, Appl
8	14	3.3	289	US-09-361-096A-47	Sequence 47, Appl
9	14	3.3	322	US-08-036-210-11	Sequence 11, Appl
10	14	3.3	322	US-08-449-609-11	Sequence 11, Appl
11	14	3.3	322	US-09-361-096A-11	Sequence 11, Appl
12	14	3.3	401	US-09-361-096A-15	Sequence 15, Appl
13	14	3.3	402	US-08-036-210-15	Sequence 15, Appl
14	14	3.3	402	US-08-449-609-15	Sequence 15, Appl
15	14	3.3	898	US-08-036-210-22	Sequence 22, Appl
16	14	3.3	898	US-08-449-609-22	Sequence 22, Appl
17	14	3.3	898	US-09-361-096A-22	Sequence 22, Appl
18	14	3.3	1501	US-08-447-464-3	Sequence 3, Appl
19	14	3.3	1501	US-08-716-679-3	Sequence 3, Appl
20	14	3.3	1911	US-08-348-006B-5	Sequence 5, Appl
21	14	3.3	1911	US-08-800-825A-5	Sequence 5, Appl
22	14	3.3	1911	US-09-158-657-5	Sequence 5, Appl
23	14	3.3	1911	PCT-US94-10166-5	Sequence 5, Appl
24	12	2.8	245	US-08-015-985-8	Sequence 8, Appl
25	12	2.8	245	US-09-280-597-8	Sequence 8, Appl
26	12	2.8	257	US-08-685-992-18	Sequence 18, Appl
27	12	2.8	257	US-09-144-925-18	Sequence 18, Appl

28	12	2.8	263	2	US-08-685-992-5	Sequence 5, Appl
29	12	2.8	263	2	US-09-144-925-5	Sequence 5, Appl
30	12	2.8	1337	3	US-08-854-585-2	Sequence 2, Appl
31	12	2.8	1337	4	US-09-447-533-2	Sequence 2, Appl
32	12	2.8	1337	5	PCT-US95-05512-2	Sequence 2, Appl
33	12	2.8	1442	1	US-08-015-986A-3	Sequence 3, Appl
34	12	2.8	1442	2	US-08-446-363-3	Sequence 3, Appl
35	12	2.8	1445	1	US-08-015-986A-2	Sequence 2, Appl
36	12	2.8	1445	2	US-08-446-363-2	Sequence 2, Appl
37	12	2.8	1711	1	US-08-342-930-2	Sequence 4, Appl
38	11	2.6	11	2	US-08-342-930-4	Sequence 4, Appl
39	11	2.6	235	1	US-08-015-985-5	Sequence 5, Appl
40	11	2.6	235	4	US-09-280-597-5	Sequence 5, Appl
41	11	2.6	236	1	US-08-015-985-6	Sequence 6, Appl
42	11	2.6	236	4	US-09-280-597-6	Sequence 6, Appl
43	11	2.6	242	1	US-08-015-985-7	Sequence 7, Appl
44	11	2.6	242	4	US-09-280-597-7	Sequence 7, Appl
45	11	2.6	248	1	US-08-015-985-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1  
US-08-446-345-34  
; Sequence 34, Application US/08446345  
; Patent No. 5831009  
; GENERAL INFORMATION:  
; APPLICANT: Ullrich, Axel  
; APPLICANT: Moller, Niels P.H.  
; APPLICANT: Moller, Karin B.  
; TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE  
; TITLE OF INVENTION: PHOSPHATASES PTF-DL  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: N.Y.  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,345  
; FILING DATE: 22-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/234,440  
; FILING DATE: 28-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30742  
; REFERENCE/DOCKET NUMBER: 7683-054  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 272 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-446-345-34

Query Match 3.5%; Score 15; DB 2; Length 272;  
Best Local Similarity 100.0%; Pred.No. 1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

354 PLLVHCSAGVGRGV 368  
|||||  
201 PLLVHCSAGVGRGV 215

RESULT 2  
S-08-446-345-36  
Sequence 36, Application US/08446345  
Patent No. 5831009  
GENERAL INFORMATION:  
APPLICANT: Ullrich, Axel  
APPLICANT: Moller, Niels P.H.  
APPLICANT: Moller, Karin B.  
TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE  
TITLE OF INVENTION: PHOSPHATASES PTP-D1  
NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: N.Y.  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446.345  
FILING DATE: 22-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/234.440  
FILING DATE: 28-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30742  
REFERENCE/DOCKET NUMBER: 7693-054  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1174 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
S-08-446-345-36

Query Match 3.5%; Score 15; DB 2; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

354 PLLVHCSAGVGRGV 368  
1103 PLLVHCSAGVGRGV 1117

RESULT 3  
S-08-036-210-9  
Sequence 9, Application US/08036210  
Patent No. 5582233  
GENERAL INFORMATION:  
APPLICANT: Moller, Niels P.H.  
APPLICANT: Moller, Karin B.  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/036,210  
FILING DATE: 23-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leelle  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 176 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-036-210-9

Query Match 3.3%; Score 14; DB 1; Length 176;  
Best Local Similarity 100.0%; Pred. No. 6.8e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCASAGVGRGVPI 370  
|||||  
DB 79 VHCASAGVGRGVPI 92

RESULT 4  
US-08-449-609-9  
Sequence 9, Application US/08449609  
Patent No. 5952212  
GENERAL INFORMATION:  
APPLICANT: Moller, Niels P.H.  
APPLICANT: Moller, Karin B.  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,609  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/036,210  
FILING DATE: 23-MAR-1993  
ATTORNEY/AGENT INFORMATION:

Query Match 3.5%; Score 15; DB 2; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

354 PLLVHCSAGVGRGV 368  
1103 PLLVHCSAGVGRGV 1117

NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-025  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 176 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
3-08-449-609-9

Query Match 3.3%; Score 14; DB 2; Length 176;  
Best Local Similarity 100.0%; Pred. No. 6.8e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCSAGVGRGTGVFI 370  
|||||  
79 VHCSAGVGRGTGVFI 92

RESULT 5  
3-09-361-096A-9  
Sequence 9, Application US/09361096A  
Patent No. 6492495  
GENERAL INFORMATION:  
APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
FILE REFERENCE: 038602/0686  
CURRENT APPLICATION NUMBER: US/09/361,096A  
CURRENT FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 08/449,609  
PRIOR FILING DATE: 1995-05-24  
PRIOR APPLICATION NUMBER: 08/036,210  
PRIOR FILING DATE: 1995-03-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 176  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: amino acid sequence  
OTHER INFORMATION: encoded by PCR fragment  
3-09-361-096A-9

Query Match 3.3%; Score 14; DB 4; Length 176;  
Best Local Similarity 100.0%; Pred. No. 6.8e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCSAGVGRGTGVFI 370  
|||||  
79 VHCSAGVGRGTGVFI 92

RESULT 6  
3-08-685-992-26  
Sequence 26, Application US/08685992  
Patent No. 5912138  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSES: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,992  
FILING DATE: 25-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 245 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-685-992-26

Query Match 3.3%; Score 14; DB 2; Length 245;  
Best Local Similarity 100.0%; Pred. No. 9.3e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCSAGVGRGTGVFI 370  
|||||  
183 VHCSAGVGRGTGVFI 196

RESULT 7  
US-09-144-925-26  
Sequence 26, Application US/09144925  
Patent No. 5951979  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSES: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02421-4799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,925  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/685,992  
FILING DATE: July 25, 1996  
ATTORNEY/AGENT INFORMATION:



NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-03Z  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 245 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
-09-144-925-26

Query Match 3.3%; Score 14; DB 2; Length 245;  
Best Local Similarity 100.0%; Pred. No. 9.3e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCSAGVGRGTGVFI 370  
183 VHCSAGVGRGTGVFI 196

RESULT 8  
-09-361-096A-47  
Sequence 47, Application US/09361096A  
Patent No. 6492495  
GENERAL INFORMATION:  
APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
FILE REFERENCE: 038602/0686  
CURRENT APPLICATION NUMBER: US/09/361,096A  
CURRENT FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 08/449,609  
PRIOR FILING DATE: 1995-05-24  
PRIOR APPLICATION NUMBER: 08/036,210  
PRIOR FILING DATE: 1995-03-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 47  
LENGTH: 289  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: PTP-S31D  
-09-361-096A-47

Query Match 3.3%; Score 14; DB 4; Length 289;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCSAGVGRGTGVFI 370  
221 VHCSAGVGRGTGVFI 234

RESULT 9  
S-08-036-210-11  
Sequence 11, Application US/08036210  
Patent No. 5585233  
GENERAL INFORMATION:  
APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS

STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/036,210  
FILING DATE: 23-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-025  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 322 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-036-210-11

Query Match 3.3%; Score 14; DB 1; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCSAGVGRGTGVFI 370  
221 VHCSAGVGRGTGVFI 234

RESULT 10  
US-08-449-609-11  
Sequence 11, Application US/08449609  
Patent No. 5952212  
GENERAL INFORMATION:  
APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,609  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7683-025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 322 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
-08-449-609-11

Query Match 3.3%; Score 14; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCAGVGRGTGVFI 370  
|||||  
221 VHCAGVGRGTGVFI 234

RESULT 11  
US-09-361-096A-11  
Sequence 11, Application US/09361096A  
Patent No. 6492495  
GENERAL INFORMATION:  
APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
FILE REFERENCE: 038602/0686  
CURRENT APPLICATION NUMBER: US/09/361,096A  
CURRENT FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 08/449,609  
PRIOR FILING DATE: 1995-05-24  
PRIOR APPLICATION NUMBER: 08/036,210  
PRIOR FILING DATE: 1995-03-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 322  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: PTP-S31D  
-09-361-096A-11

Query Match 3.3%; Score 14; DB 4; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCAGVGRGTGVFI 370  
|||||  
221 VHCAGVGRGTGVFI 234

RESULT 12  
US-09-361-096A-15  
Sequence 15, Application US/09361096A  
Patent No. 6492495  
GENERAL INFORMATION:  
APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
FILE REFERENCE: 038602/0686  
CURRENT APPLICATION NUMBER: US/09/361,096A  
CURRENT FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 08/449,609  
PRIOR FILING DATE: 1995-05-24  
PRIOR APPLICATION NUMBER: 08/036,210

PRIOR FILING DATE: 1995-03-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 401  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-361-096A-15

Query Match 3.3%; Score 14; DB 4; Length 401;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCAGVGRGTGVFI 370  
|||||  
300 VHCAGVGRGTGVFI 313

RESULT 13  
US-08-036-210-15  
Sequence 15, Application US/08036210  
Patent No. 5585233  
GENERAL INFORMATION:  
APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
FILE REFERENCE: 038602/0686  
CURRENT APPLICATION NUMBER: US/08/036,210  
CURRENT FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 08/449,609  
PRIOR FILING DATE: 1995-05-24  
PRIOR APPLICATION NUMBER: 08/036,210  
PRIOR FILING DATE: 1995-03-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
SEQ ID NO 15  
LENGTH: 401  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: PTP-S31D  
-08-036-210-15

Query Match 3.3%; Score 14; DB 1; Length 402;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCAGVGRGTGVFI 370  
|||||  
301 VHCAGVGRGTGVFI 314

RESULT 14  
US-08-449-609-15  
Sequence 15, Application US/08449609

Patent No. 5952212  
GENERAL INFORMATION:  
APPLICANT: Moller, Niels P.H.  
APPLICANT: Moller, Karin B.  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,609  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: US 08/036,210  
FILING DATE: 23-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-025  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 402 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
1-08-449-609-15

Query Match 3.3%; Score 14; DB 2; Length 402;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCSAGVGRGTGVFI 370  
|||||  
301 VHCSAGVGRGTGVFI 314

RESULT 15  
3-08-036-210-22  
Sequence 22, Application US/08036210  
Patent No. 5585233  
GENERAL INFORMATION:  
APPLICANT: Moller, Niels P.H.  
APPLICANT: Moller, Karin B.  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/036,210  
FILING DATE: 23-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 898 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-036-210-22

Query Match 3.3%; Score 14; DB 1; Length 898;  
Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTGVFI 370  
|||||  
DB 797 VHCSAGVGRGTGVFI 810

Search completed: June 16, 2004, 13:34:07  
Job time : 24 secs

GenCore version 5.1.6  
 Copyright (c) 1993 - 2004 Compugen Ltd.

! protein - protein search, using sw model

on: June 16, 2004, 13:33:02 ; Search time 48 Seconds  
 (without alignments)  
 2500.319 Million cell updates/sec

tle: US-09-095-478A-5  
 rfect score: 426  
 quence: 1 MSSPRKVRGKTGRDNDEEG.....QYQFCYEIVLEVLQNLALY 426

oring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

arched: 1158786 seqs, 281726120 residues

rd size : 0

tal number of hits satisfying chosen parameters: 1158786

nimum DB seq length: 0

ximum DB seq length: 2000000000

st-processing: Listing first 45 summaries

tabase : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

sult No.	Score	Query Length	ID	Description
1	426	100.0	426 10	US-09-095-478-1 Sequence 1, Appli
2	405	95.1	412 10	US-09-095-478-3 Sequence 3, Appli
3	383	89.9	463 10	US-09-095-478-2 Sequence 2, Appli
4	379	89.0	379 10	US-09-095-478-8 Sequence 8, Appli
5	354	83.1	354 10	US-09-095-478-6 Sequence 6, Appli
6	122	28.6	122 10	US-09-095-478-4 Sequence 4, Appli
7	30	7.0	30 10	US-09-095-478-22 Sequence 22, Appl
8	29	6.8	29 10	US-09-095-478-23 Sequence 23, Appl
9	29	6.8	29 10	US-09-095-478-24 Sequence 24, Appl
10	29	6.8	29 10	US-09-095-478-25 Sequence 25, Appl
11	23	5.4	122 10	US-09-095-478-5 Sequence 5, Appli
12	19	4.5	420 16	US-10-311-764-4 Sequence 4, Appli
13	15	3.5	1105 12	US-10-296-115-1082 Sequence 1082, Ap
14	14	3.3	162 15	US-10-334-143-191 Sequence 191, App
15	14	3.3	176 14	US-10-314-232-9 Sequence 9, Appli

15	14	3.3	289	14	US-10-314-232-47	Sequence 47, Appl
17	14	3.3	294	9	US-09-788-826-27	Sequence 27, Appl
18	14	3.3	322	14	US-10-314-232-11	Sequence 11, Appl
19	14	3.3	344	16	US-10-408-765A-1670	Sequence 1670, Ap
20	14	3.3	401	14	US-10-314-232-15	Sequence 15, Appl
21	14	3.3	442	9	US-09-925-300-950	Sequence 950, App
22	14	3.3	647	15	US-10-291-265-722	Sequence 722, App
23	14	3.3	898	14	US-10-314-232-22	Sequence 22, Appl
24	14	3.3	1495	15	US-10-253-666-12	Sequence 12, Appl
25	14	3.3	1502	9	US-09-808-602-54	Sequence 54, Appl
26	14	3.3	1502	10	US-09-800-198-44	Sequence 44, Appl
27	14	3.3	1907	15	US-10-291-265-250	Sequence 250, App
28	14	3.3	1948	9	US-09-808-602-55	Sequence 55, Appl
29	14	3.3	1948	10	US-09-800-198-45	Sequence 45, Appl
30	14	3.3	2281	12	US-10-087-684-6	Sequence 6, Appli
31	14	3.3	2281	12	US-10-218-779-6	Sequence 6, Appli
32	14	3.3	2291	10	US-09-822-871-2	Sequence 2, Appli
33	14	3.3	2291	16	US-10-673-885-2	Sequence 2, Appli
34	14	3.3	2299	16	US-10-466-759-2	Sequence 2, Appli
35	14	3.3	2300	12	US-10-087-684-10	Sequence 10, Appl
36	14	3.3	2300	12	US-10-218-779-10	Sequence 10, Appl
37	14	3.3	2301	10	US-09-822-871-4	Sequence 4, Appli
38	14	3.3	2301	16	US-10-673-885-4	Sequence 4, Appli
39	14	3.3	2302	12	US-10-087-684-37	Sequence 37, Appl
40	14	3.3	2302	12	US-10-218-779-37	Sequence 37, Appl
41	12	2.8	313	9	US-09-788-626-19	Sequence 19, Appl
42	12	2.8	319	9	US-09-788-626-6	Sequence 6, Appli
43	12	2.8	1216	15	US-10-366-547-49	Sequence 49, Appl
44	12	2.8	1238	15	US-10-366-547-47	Sequence 47, Appl
45	12	2.8	1329	16	US-10-408-765A-2747	Sequence 2747, Ap

## ALIGNMENTS

## RESULT 1

US-09-095-478-1  
 ; Sequence 1, Application US/09095478  
 ; Publication No. US20030095970A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Plowman, Gregory  
 ; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
 ; TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND  
 ; TITLE OF INVENTION: RELATED PRODUCTS AND  
 ; TITLE OF INVENTION: METHODS  
 ; NUMBER OF SEQUENCES: 25  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; CITY: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FastSeq for Windows 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/095,478  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 224/115  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 426 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 S-09-095-478-1

Query Match 100.0%; Score 426; DB 10; Length 426;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSSPRKVRGKTGRDNDEBEGSGNLNLSLPSSSQKMTPTKPIFGNKNSENKVPKSHL 60  
 1 MSSPRKVRGKTGRDNDEBEGSGNLNLSLPSSSQKMTPTKPIFGNKNSENKVPKSHL 60  
 61 SFSDKYELVYPPLESDDTETVWVSDSLRNRNWMDSETAGPSKTVSPVLSGSSRLSK 120  
 61 SFSDKYELVYPPLESDDTETVWVSDSLRNRNWMDSETAGPSKTVSPVLSGSSRLSK 120  
 121 DTETSVSEKELTQIAQIRPLIFNSSARSAMRDCLNTLQKKEELDIIRFLELEQMTLPDD 180  
 121 DTETSVSEKELTQIAQIRPLIFNSSARSAMRDCLNTLQKKEELDIIRFLELEQMTLPDD 180  
 181 FNSGNTLQNRDQNRVLDLPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPE 240  
 181 FNSGNTLQNRDQNRVLDLPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPE 240  
 241 TTEDFWQVLENNCNVIAITREIECGVICKYSYWPISLKEPFEHFSVFLETFHVTQY 300  
 241 TTEDFWQVLENNCNVIAITREIECGVICKYSYWPISLKEPFEHFSVFLETFHVTQY 300  
 301 FTVRVFIQVKSTGKSCVKKHLOFTKPDHGTASADFFIKYVYVRKSHITGPLLHVC 360  
 301 FTVRVFIQVKSTGKSCVKKHLOFTKPDHGTASADFFIKYVYVRKSHITGPLLHVC 360  
 361 AGVGTGVFICVDVWVPSAEIKNSYFDINNIVTOMRKORCGMIQTK 420  
 361 AGVGTGVFICVDVWVPSAEIKNSYFDINNIVTOMRKORCGMIQTK 420  
 421 NULLY 426  
 421 NULLY 426

## RESULT 2

S-09-095-478-3

Sequence 3, Application US/09095478

Publication No. US20030095970A1

GENERAL INFORMATION:

APPLICANT: Plowman, Gregory

TITLE OF INVENTION: NOVEL PROTEIN TYROSINE

TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND

TITLE OF INVENTION: RELATED PRODUCTS AND

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESS: Lyon &amp; Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq for Windows 2.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/095,478  
 FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 224/115

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 412 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide  
 S-09-095-478-3

Query Match 95.1%; Score 405; DB 10; Length 412;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSPRKVRGKTGRDNDEBEGSGNLNLSLPSSSQKMTPTKPIFGNKNSENKVPKSHL 60  
 DB 1 MSSPRKVRGKTGRDNDEBEGSGNLNLSLPSSSQKMTPTKPIFGNKNSENKVPKSHL 60  
 QY 61 SFSDKYELVYPPLESDDTETVWVSDSLRNRNWMDSETAGPSKTVSPVLSGSSRLSK 120  
 DB 61 SFSDKYELVYPPLESDDTETVWVSDSLRNRNWMDSETAGPSKTVSPVLSGSSRLSK 120  
 QY 121 DTETSVSEKELTQIAQIRPLIFNSSARSAMRDCLNTLQKKEELDIIRFLELEQMTLPDD 180  
 DB 121 DTETSVSEKELTQIAQIRPLIFNSSARSAMRDCLNTLQKKEELDIIRFLELEQMTLPDD 180  
 QY 181 FNSGNTLQNRDQNRVLDLPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPE 240  
 DB 181 FNSGNTLQNRDQNRVLDLPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPE 240  
 QY 241 TTEDFWQVLENNCNVIAITREIECGVICKYSYWPISLKEPFEHFSVFLETFHVTQY 300  
 DB 241 TTEDFWQVLENNCNVIAITREIECGVICKYSYWPISLKEPFEHFSVFLETFHVTQY 300  
 QY 301 FTVRVFIQVKSTGKSCVKKHLOFTKPDHGTASADFFIKYVYVRKSHITGPLLHVC 360  
 DB 301 FTVRVFIQVKSTGKSCVKKHLOFTKPDHGTASADFFIKYVYVRKSHITGPLLHVC 360  
 QY 361 AGVGTGVFICVDVWVPSAEIKNSYFDINNIVTOMRKORCGMIQTK 405  
 DB 361 AGVGTGVFICVDVWVPSAEIKNSYFDINNIVTOMRKORCGMIQTK 405

## RESULT 3

US-095-478-2

Sequence 2, Application US/09095478

Publication No. US20030095970A1

GENERAL INFORMATION:

APPLICANT: Plowman, Gregory

TITLE OF INVENTION: NOVEL PROTEIN TYROSINE

TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND

TITLE OF INVENTION: RELATED PRODUCTS AND

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon &amp; Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSEQ for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 463 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
-09-095-478-2

Query Match 89.9%; Score 383; DB 10; Length 463;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

44 IFGNKMSNVKPSHLSFSDKYELVYPEPLESDTDTVDVSDSLRNKNSMDSETAG 103  
81 IFGNKMSNVKPSHLSFSDKYELVYPEPLESDTDTVDVSDSLRNKNSMDSETAG 140  
104 PSKTVSPVLSSGSSRLSKDTETSVSEKELTQLAIRPLIFNSSARSAMRDCNLTKKEBL 163  
141 PSKTVSPVLSSGSSRLSKDTETSVSEKELTQLAIRPLIFNSSARSAMRDCNLTKKEBL 200  
164 DIREFLEQMTLPDDFNSGNTLQNRDKNYRDILPYDSTRVPLGKNKDYINASTIRIV 223  
201 DIREFLEQMTLPDDFNSGNTLQNRDKNYRDILPYDSTRVPLGKNKDYINASTIRIV 260  
224 NHEEYFYIATQGPLPETIEDFWQVLENNCNVMIATREIECGVIKCYSWPISLKEPL 283  
261 NHEEYFYIATQGPLPETIEDFWQVLENNCNVMIATREIECGVIKCYSWPISLKEPL 320  
284 EPEHPSVLETFHTVQYPTVRVFOIVKSTGKSCVKGHLOFTKWPDHGTPASADFFIKYV 343  
321 EPEHPSVLETFHTVQYPTVRVFOIVKSTGKSCVKGHLOFTKWPDHGTPASADFFIKYV 380  
344 RYVRKSHITGPLLHVCAGVGRGTGVFCVDVVFSAIEKNYSFDIMNIVTQMKQRCGMIO 403  
381 RYVRKSHITGPLLHVCAGVGRGTGVFCVDVVFSAIEKNYSFDIMNIVTQMKQRCGMIO 440  
404 TREQYQFCYEIVLEVLQNLALY 426  
441 TREQYQFCYEIVLEVLQNLALY 463

;SULT 4

-09-095-478-8  
Sequence 8, Application US/09095478  
Publication No. US20030095970A1  
GENERAL INFORMATION:  
APPLICANT: Pflomman, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE

TITLE OF INVENTION: PHOSPHATASE SUPTPO5 AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
METHODS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
CITY: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSEQ for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 379 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-095-478-8

Query Match 89.0%; Score 379; DB 10; Length 379;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 GNKMSNVKPSHLSFSDKYELVYPEPLESDTDTVDVSDSLRNKNSMDSETAGPS 105  
DB 1 GNKMSNVKPSHLSFSDKYELVYPEPLESDTDTVDVSDSLRNKNSMDSETAGPS 60  
QY 106 KTVSPVLSSGSSRLSKDTETSVSEKELTQLAIRPLIFNSSARSAMRDCNLTKKEBLDI 165  
DB 61 KTVSPVLSSGSSRLSKDTETSVSEKELTQLAIRPLIFNSSARSAMRDCNLTKKEBLDI 120  
QY 166 IREFLEQMTLPDDFNSGNTLQNRDKNYRDILPYDSTRVPLGKNKDYINASTIRIVNH 225  
DB 121 IREFLEQMTLPDDFNSGNTLQNRDKNYRDILPYDSTRVPLGKNKDYINASTIRIVNH 180  
QY 226 EEEFYIATQGPLPETIEDFWQVLENNCNVMIATREIECGVIKCYSWPISLKEPLEF 285  
DB 181 EEEFYIATQGPLPETIEDFWQVLENNCNVMIATREIECGVIKCYSWPISLKEPLEF 240  
QY 286 EPEHPSVLETFHTVQYPTVRVFOIVKSTGKSCVKGHLOFTKWPDHGTPASADFFIKYV 345  
DB 241 EPEHPSVLETFHTVQYPTVRVFOIVKSTGKSCVKGHLOFTKWPDHGTPASADFFIKYV 300  
QY 346 VRKSHITGPLLHVCAGVGRGTGVFCVDVVFSAIEKNYSFDIMNIVTQMKQRCGMIO 405  
DB 301 VRKSHITGPLLHVCAGVGRGTGVFCVDVVFSAIEKNYSFDIMNIVTQMKQRCGMIO 360  
QY 406 EYQFCYEIVLEVLQNLALY 424  
DB 361 EYQFCYEIVLEVLQNLALY 379

35ULT 5

3-09-095-478-6  
Sequence 6, Application US/09095478  
Publication No. US20030095970A1  
GENERAL INFORMATION:  
APPLICANT: Plowman, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSEQ for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 354 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
3-09-095-478-6

Query Match 83.1%; Score 354; DB 10; Length 354;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

71 PEPLESDTDTWVDSRLNRNNSMDSETAGPSKTVSPVLGSGSLSKDTSVSEKE 130  
1 PEPLESDTDTWVDSRLNRNNSMDSETAGPSKTVSPVLGSGSLSKDTSVSEKE 60  
131 LTQLAQIPLIENSSARSAMRDCLNTLQKKEELDIIRFLELEQWTLDPDFNSGNTLQNR 190  
61 LTQLAQIPLIENSSARSAMRDCLNTLQKKEELDIIRFLELEQWTLDPDFNSGNTLQNR 120  
191 DKNRYRDLPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGLPETIEDFMQVL 250  
121 DKNRYRDLPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGLPETIEDFMQVL 180  
251 ENNCNVIAMITREICGVTKCYSWPISLKEPLFEHFSVLETFHVTQYFTV 310  
181 ENNCNVIAMITREICGVTKCYSWPISLKEPLFEHFSVLETFHVTQYFTV 240  
311 KSTGKSCQVKHLQFTKWPDHGTPASADFFIKYRVYVRKSHITGPELLVHCAGVGRGTGVP 370

Db 241 KSTGKSCQVKHLQFTKWPDHGTPASADFFIKYRVYVRKSHITGPELLVHCAGVGRGTGVP 300  
Qy 371 CVDVVFSAIERKNSYFDINNIIVTQMRKORCGMIQTKQYQFCYHIVLEVLQNLLA 424  
Db 301 CVDVVFSAIERKNSYFDINNIIVTQMRKORCGMIQTKQYQFCYHIVLEVLQNLLA 354

## RESULT 6

US-09-095-478-4  
Sequence 4, Application US/09095478  
Publication No. US20030095970A1  
GENERAL INFORMATION:  
APPLICANT: Plowman, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSEQ for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-095-478-4

Query Match 28.6%; Score 122; DB 10; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.5e-112;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

244 DFWQVLENNCNVIAITREIECGVTKCYSWPISLKEPLFEHFSVLETFHVTQYFTV 303  
1 DFWQVLENNCNVIAITREIECGVTKCYSWPISLKEPLFEHFSVLETFHVTQYFTV 60  
304 RVFQIVKSTGKSCQVKHLQFTKWPDHGTPASADFFIKYRVYVRKSHITGPELLVHCAGV 363  
61 RVFQIVKSTGKSCQVKHLQFTKWPDHGTPASADFFIKYRVYVRKSHITGPELLVHCAGV 120

Qy 244 DFWQVLENNCNVIAITREIECGVTKCYSWPISLKEPLFEHFSVLETFHVTQYFTV 303  
Db 1 DFWQVLENNCNVIAITREIECGVTKCYSWPISLKEPLFEHFSVLETFHVTQYFTV 60  
Qy 304 RVFQIVKSTGKSCQVKHLQFTKWPDHGTPASADFFIKYRVYVRKSHITGPELLVHCAGV 363  
Db 61 RVFQIVKSTGKSCQVKHLQFTKWPDHGTPASADFFIKYRVYVRKSHITGPELLVHCAGV 120  
Qy 364 GR 365  
Db 121 GR 122

## RESULT 7

-09-095-478-22  
 Sequence 22, Application US/09095478  
 Publication No. US20030095970A1  
 GENERAL INFORMATION:  
 APPLICANT: Plowman, Gregory  
 TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
 TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND  
 TITLE OF INVENTION: RELATED PRODUCTS AND  
 TITLE OF INVENTION: METHODS  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSEQ for Windows 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/095,478  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 224/115  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 22:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 30 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 -09-095-478-22

Query Match 7.0%; Score 30; DB 10; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-22;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

176 TLPDPSGNTLQNRDKRYRDLIPYDSTR 205  
 1 TLPDPSGNTLQNRDKRYRDLIPYDSTR 30

## SULT 8

-09-095-478-23  
 Sequence 23, Application US/09095478  
 Publication No. US20030095970A1  
 GENERAL INFORMATION:  
 APPLICANT: Plowman, Gregory  
 TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
 TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND  
 TITLE OF INVENTION: RELATED PRODUCTS AND  
 TITLE OF INVENTION: METHODS  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700

CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSEQ for Windows 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/095,478  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 224/115  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 23:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 29 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 US-09-095-478-23

Query Match 6.8%; Score 29; DB 10; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-21;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSPKRVKGTGRDNDDEEGNSGNLNLRN 29  
 DB 1 MSSPKRVKGTGRDNDDEEGNSGNLNLRN 29

## RESULT 9

US-09-095-478-24  
 Sequence 24, Application US/09095478  
 Publication No. US20030095970A1  
 GENERAL INFORMATION:

APPLICANT: Plowman, Gregory  
 TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
 TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND  
 TITLE OF INVENTION: RELATED PRODUCTS AND  
 TITLE OF INVENTION: METHODS  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSEQ for Windows 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/095,478  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:



```
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-09-095-478-24

Query Match 6.8%; Score 29; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 6.9e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

109 SPVLSGSRSLKQDTSVSEKELTQLAQI 137
|||||
1 SPVLSGSRSLKQDTSVSEKELTQLAQI 29

RESULT 10
US-09-095-478-25
Sequence 25, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPTPOS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-09-095-478-25

Query Match 5.4%; Score 23; DB 10; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

337 DFFIKYVYVRKSHITGELLVHC 359
|||||
94 DFFIKYVYVRKSHITGELLVHC 116

RESULT 12
US-10-311-764-4
```

Sequence 4, Application US/10311764  
Publication No. US20040023245A1  
GENERAL INFORMATION:  
APPLICANT: INCYTE GENOMICS, INC.; AU-YOUNG, Janice K.  
APPLICANT: BAUGHN, Mariah R.; DING, Li  
APPLICANT: ELLIOTT, Vicki S.; GANDHI, Ameena R.  
APPLICANT: GRIFFIN, Jennifer A.; HAPALIA, April J.A.  
APPLICANT: KEARNEY, Liam; LEE, Ernestine A.  
APPLICANT: LU, Yan; NGUYEN, Darniel B.  
APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi  
APPLICANT: REDDY, Roopa M.; SANJANWALA, Madhusudan M.  
APPLICANT: STEWART, Elizabeth A.; TANG, Y. Tom  
APPLICANT: THORNTON, Michael B.; TRIBOULEY, Catherine M.  
APPLICANT: CHAWLA, Narinder K.; YANG, Junming  
APPLICANT: YAO, Monique G.; YUE, Henry  
TITLE OF INVENTION: PROTEIN PHOSPHATASES  
FILE REFERENCE: PI-0126 USN  
CURRENT APPLICATION NUMBER: US/10/311,764  
CURRENT FILING DATE: 2002-12-16  
PRIOR APPLICATION NUMBER: PCT/US01/19442  
PRIOR FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: US 60/212,447  
PRIOR FILING DATE: 2000-06-16  
PRIOR APPLICATION NUMBER: US 60/213,746  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: US 60/215,210  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: US 60/216,529  
PRIOR FILING DATE: 2000-07-06  
PRIOR APPLICATION NUMBER: US 60/218,080  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/220,117  
PRIOR FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PERL Program  
SEQ ID NO 4  
LENGTH: 420  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. US20040023245A1 7476861CD1  
->10-311-764-4

Query Match 4.5%; Score 19; DB 16; Length 420;  
Best Local Similarity 100.0%; Pred. No. 6.4e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

192 KNYRDILPYDSTRVPLCK 210  
186 KNYRDILPYDSTRVPLCK 204

RESULT 13  
->10-296-115-1082  
Sequence 1082, Application US/10296115  
Publication No. US20040053248A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq Inc  
TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides  
FILE REFERENCE: 784PCT  
CURRENT APPLICATION NUMBER: US/10/296,115  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: US09/488,725  
PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: US09/552,317  
PRIOR FILING DATE: 2000-04-25  
NUMBER OF SEQ ID NOS: 1478  
SEQ ID NO 1082  
LENGTH: 1105  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:

NAME/KEY: misc feature  
LOCATION: (1)...(1105)  
OTHER INFORMATION: Xaa = any amino acid or other as shown in Table 3  
US-10-296-115-1082

Query Match 3.5%; Score 15; DB 12; Length 1105;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 PLLVHCSAGVGRGV 368  
Db 1015 PLLVHCSAGVGRGV 1029

RESULT 14  
US-10-334-143-191  
Sequence 191, Application US/10334143  
Publication No. US20040009549A1  
GENERAL INFORMATION:  
APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH  
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL  
TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD  
FILE REFERENCE: 038602/1543  
CURRENT APPLICATION NUMBER: US/10/334,143  
CURRENT FILING DATE: 2002-12-31  
PRIOR APPLICATION NUMBER: 60/343,169  
PRIOR FILING DATE: 2001-12-31  
NUMBER OF SEQ ID NOS: 207  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 191  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Unknown Organism  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: 11arA protein sequence  
US-10-334-143-191

Query Match 3.3%; Score 14; DB 15; Length 162;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGV 370  
Db 103 VHCAGVGRGV 116

RESULT 15  
US-10-314-232-9  
Sequence 9, Application US/10314232  
Publication No. US20030138932A1  
GENERAL INFORMATION:  
APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
FILE REFERENCE: 038602/0686  
CURRENT APPLICATION NUMBER: US/10/314,232  
CURRENT FILING DATE: 2002-12-09  
PRIOR APPLICATION NUMBER: US/09/361,096  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 08/449,609  
PRIOR FILING DATE: 1995-05-24  
PRIOR APPLICATION NUMBER: 08/036,210  
PRIOR FILING DATE: 1995-03-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 176  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: amino acid sequence

OTHER INFORMATION: encoded by PCR fragment  
S-10-314-232-9

Query Match 3.3%; Score 14; DB 14; Length 176;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 357 VHCSAGVGRGVPI 370  
b 79 VHCSAGVGRGVPI 92

earch completed: June 16, 2004, 13:38:58  
ob time : 49 secs

GenCore version 5.1.6  
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1 protein - protein search, using sw model

in on: June 16, 2004, 13:29:21 ; Search time 20 Seconds  
(without alignments)  
2048.880 Million cell updates/sec

tle: US-09-095-478A-5  
ffect score: 426  
quence: 1 MSSPRKVRGKTGRNDDEEG.....QYQFCVEIVLEVLQNLALY 426

oring table: OLIGO  
Gapop 60.0 , Gapext 60.0

arched: 283366 seqs, 96191526 residues

rd size : 0

ital number of hits satisfying chosen parameters: 283366

nimum DB seq length: 0  
ximum DB seq length: 2000000000

st-processing: Listing first 45 summaries

tabase : PIR 78:\*  
1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	ID	Description
1	19	4.5	398	2 T08716	protein-tyrosine-p
2	15	3.5	1174	2 I38140	protein-tyrosine-p
3	15	3.5	1175	2 S51005	protein-tyrosine-p
4	15	3.5	1176	2 I58345	protein tyrosine-p
5	14	3.3	582	2 A57068	protein-tyrosine-p
6	14	3.3	1231	2 S53089	protein-tyrosine-p
7	14	3.3	1290	2 A56493	leucocyte common a
8	14	3.3	1496	1 A48758	protein-tyrosine-p
9	14	3.3	1499	2 I50212	protein-tyrosine-p
10	14	3.3	1501	2 I58148	protein-tyrosine-p
11	14	3.3	1691	1 D54689	protein-tyrosine-p
12	14	3.3	1863	2 S46217	protein-tyrosine-p
13	14	3.3	1894	2 S54689	protein-tyrosine-p
14	14	3.3	1897	1 T0HULX	leukocyte antigen-
15	14	3.3	1898	2 S46216	leukocyte antigen-
16	14	3.3	1907	2 S50893	protein-tyrosine-p
17	14	3.3	1912	2 A36178	protein-tyrosine-p
18	14	3.3	2051	2 T30938	receptor tyrosine
19	14	3.3	2302	2 T14328	protein-tyrosine-p
20	12	2.8	184	2 T15125	hypothetical prote
21	12	2.8	1187	1 J41155	protein-tyrosine-p
22	12	2.8	1189	1 J23466	protein-tyrosine-p
23	12	2.8	1217	2 T22672	hypothetical prote
24	12	2.8	1238	2 S68700	HPTP beta-like tyr
25	12	2.8	1337	1 I38670	protein-tyrosine-p
26	12	2.8	1442	1 B48148	protein-tyrosine-p
27	12	2.8	1445	1 A48148	protein-tyrosine-p
28	12	2.8	1462	1 B36182	protein-tyrosine-p
29	12	2.8	1711	1 A55148	protein-tyrosine-p

30	11	2.6	198	2 T27722	hypothetical prote
31	11	2.6	256	2 A40169	protein-tyrosine-p
32	11	2.6	335	1 A39862	protein-tyrosine-p
33	11	2.6	398	2 I56540	protein-tyrosine-p
34	11	2.6	405	2 I49372	protein-tyrosine-p
35	11	2.6	405	2 S68250	protein-tyrosine-p
36	11	2.6	483	2 T25992	hypothetical prote
37	11	2.6	521	1 A44267	protein-tyrosine-p
38	11	2.6	550	1 A40449	protein-tyrosine-p
39	11	2.6	583	2 S17671	protein-tyrosine-p
40	11	2.6	699	2 J06132	protein-tyrosine-p
41	11	2.6	700	1 S12053	protein-tyrosine-p
42	11	2.6	711	1 S28391	protein-tyrosine-p
43	11	2.6	796	1 J01285	protein-tyrosine-p
44	11	2.6	802	1 A36065	protein-tyrosine-p
45	11	2.6	829	1 A47373	protein-tyrosine-p

ALIGNMENTS

RESULT 1

T08716  
protein-tyrosine-phosphatase homolog DKFZp566K0524.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 13-Aug-1999  
C:Accession: T08716  
R:Ansoorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, May 1999  
A:Reference number: Z16472  
A:Accession: T08716  
A:Molecule type: mRNA  
A:Residues: 1-398 <ANS>  
A:Cross-references: EMBL:AL050040  
A:Experimental source: fetal kidney; clone DKFZp566K0524  
C:Genetics:  
A:Note: DKFZp566K0524.1  
C:Superfamily: protein-tyrosine-phosphatase homology  
F:161-379/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 4.5%; Score 19; DB 2; Length 398;  
Best Local Similarity 100.0%; Pred. No. 3.6e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	132	KNYRDILPYDSTRVPLGK	210
DB	164	KNYRDILPYDSTRVPLGK	182

RESULT 2

I38140  
protein-tyrosine-phosphatase (EC 3.1.3.48) - human  
C:Species: Homo sapiens (man)  
C:Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 22-Jun-1999  
C:Accession: I38140  
R:Moller, N.P.; Moller, K.B.; Lammers, R.; Kharitonkov, A.; Sures, I.; Ullrich, A.  
Proc. Natl. Acad. Sci. U.S.A. 91, 7477-7481, 1994  
A:Title: Src kinase associates with a member of a distinct subfamily of protein-tyrosine  
A:Reference number: I38140; MUID:94329538; PMID:7519780  
A:Accession: I38140  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1174 <RES>  
A:Cross-references: EMBL:X79510; NID:G532055; PIDN:CAA56042.1; PID:G532056  
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-b;  
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas  
F:25-304/Domain: protein 4.1 membrane-binding domain homology <B41>  
F:921-1156/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F:1108/Active site: Cys [phosphocysteine intermediate] #status Predicted  
F:1114/Binding site: substrate phosphate (Arg) #status Predicted  
Query Match 3.5%; Score 15; DB 2; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 1.4e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 354 PLLVHCSAGVGRGV 368  
 |||||  
 b 1103 PLLVHCSAGVGRGV 1117  
 |||||

RESULT 3

S1005  
 protein-tyrosine-phosphatase (EC 3.1.3.48) 2E - rat  
 ;Species: Rattus norvegicus (Norway rat)  
 ;Date: 10-Apr-1996 #sequence\_revision 03-May-1996 #text\_change 22-Jun-1999  
 ;Accession: S51005; S51161  
 ;Alphabet: D.; Banyville, D.; Tong, Y.; Stocco, R.; Masson, S.; Ma, S.; Fantus, G.; Shen, B.S. Lett. 367, 351-356, 1994  
 ;Title: Identification of a novel protein tyrosine phosphatase with sequence homology to the protein-tyrosine phosphatase family  
 ;Reference number: S51005; MUID:95104449; PMID:7805671  
 ;Accession: S51005  
 ;Molecule type: mRNA  
 ;Residues: 1-1175 <LAA>  
 ;Cross-references: EMBL:U17971; NID:g662113; PIDN:AAA62153.1; PID:g602255  
 ;Genetics: PTP2E  
 ;Accession: S51161  
 ;Molecule type: mRNA  
 ;Residues: 840-1175 <LAA>  
 ;Cross-references: EMBL:U18293; NID:g603228; PIDN:AAA62154.1; PID:g603229  
 ;Genetics: PTP2E1  
 ;Note: clone PTP2E  
 ;Genetics: <PTP2E1>  
 ;Note: clone PTP2E1  
 ;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-b  
 ;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
 ;25-304/Domain: protein 4.1 membrane-binding domain homology <B41>  
 ;922-1157/Domain: protein-tyrosine-phosphatase homology <PTP2>  
 ;1109/Active site: Cys (phosphocysteine intermediate) #status predicted  
 ;1115/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.5%; Score 15; DB 2; Length 1175;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 354 PLLVHCSAGVGRGV 368  
 |||||  
 b 1104 PLLVHCSAGVGRGV 1118  
 |||||

RESULT 4

S8345  
 protein tyrosine phosphatase - mouse  
 ;Species: Mus musculus (house mouse)  
 ;Date: 28-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 22-Jun-1999  
 ;Accession: I58345  
 ;Alphabet: S.; Higashitsuji, H.; Arii, S.; Furutani, M.; Imamura, M.; Kaneko, Y.; Takenawa, J.; Nakay  
 ;Title: Enhanced expression of multiple protein tyrosine phosphatases in the regenerati  
 ;Reference number: I58345; MUID:95140431; PMID:7839537  
 ;Accession: I58345  
 ;Status: preliminary; translated from GB/EMBL/DDJ  
 ;Molecule type: mRNA  
 ;Residues: 1-1176 <RES>  
 ;Cross-references: GB:D37801; NID:g604885; PIDN:BAA07053.1; PID:g604886  
 ;Genetics:  
 ;Gene: PTP-PL10  
 ;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-b  
 ;Keywords: phosphoprotein  
 ;25-304/Domain: protein 4.1 membrane-binding domain homology <B41>  
 ;923-1158/Domain: protein-tyrosine-phosphatase homology <PTP2>  
 ;1110/Active site: Cys (phosphocysteine intermediate) #status predicted  
 ;1116/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.5%; Score 15; DB 2; Length 1176;

Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 PLLVHCSAGVGRGV 368  
 |||||  
 DB 1105 PLLVHCSAGVGRGV 1119  
 |||||

RESULT 5

A57068  
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type f - mouse (fragment)  
 ;Alternate names: leukocyte antigen-related protein LAR  
 ;Species: Mus musculus (house mouse)  
 ;Date: 03-Oct-1995 #sequence\_revision 09-Mar-1996 #text\_change 23-Jul-1999  
 ;Accession: A57068; S40280  
 ;Schapaveld, R.O.J.; van den Maagdenberg, A.M.J.M.; Schepens, J.T.G.; Olde Weghuis, D.;  
 ;Title: The mouse gene Ptpfr encoding the leukocyte common antigen-related molecule LAR  
 ;Reference number: A57068; MUID:95394448; PMID:7665159  
 ;Accession: A57068  
 ;Status: not compared with conceptual translation  
 ;Molecule type: mRNA  
 ;Residues: 1-582 <SCH>  
 ;Cross-references: GB:D37988; NID:g993005; PIDN:CAA86070.1; PID:g993006  
 ;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.  
 ;Submitted to the EMBL Data Library, June 1993  
 ;Description: Assessment of the expression levels of murine protein-tyrosine phosphatase  
 ;Reference number: S40280  
 ;Accession: S40280  
 ;Molecule type: mRNA  
 ;Residues: 116-221 <HEN>  
 ;Cross-references: EMBL:Z23049; NID:g438135; PIDN:CAA80584.1; PID:g438136  
 ;Genetics:  
 ;Gene: Ptpfr  
 ;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; i  
 ;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane f  
 ;F1-582/Domain: leukocyte common antigen cytosolic domain homology (fragment) <LAC>  
 ;F339-562/Domain: protein-tyrosine-phosphatase homology <PTP1>  
 ;F223/Active site: Cys (phosphocysteine intermediate) #status predicted  
 ;F229/Binding site: substrate phosphate (Arg) #status predicted  
 ;F514/Active site: Cys (phosphocysteine intermediate) #status predicted  
 ;F520/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.3%; Score 14; DB 2; Length 582;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGV 370  
 |||||  
 DB 512 VHCAGVGRGV 525  
 |||||

RESULT 6

S53089  
 protein-tyrosine-phosphatase (EC 3.1.3.48) AnLAR - African malaria mosquito (fragment)  
 ;Alternate names: leukocyte antigen-related protein  
 ;Species: Anopheles gambiae (African malaria mosquito)  
 ;Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
 ;Accession: S53089  
 ;Spier, S.  
 ;Submitted to the EMBL Data Library, March 1995  
 ;Description: Anlar-a transmembrane, receptor-like protein tyrosine phosphatase from the  
 ;Reference number: S53089  
 ;Accession: S53089  
 ;Molecule type: DNA  
 ;Residues: 1-1231 <SP1>  
 ;Cross-references: EMBL:X85217; NID:g732549; PIDN:CAA59483.1; PID:g732550  
 ;Genetics:  
 ;Introns: 1026/3; 1070/3; 1209/3  
 ;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; i  
 ;Keywords: leukocyte antigen-related protein; fibronectin type III repeat homology; i

Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane  
 208-293/Domain: fibronectin type III repeat homology <3PR>  
 619-1231/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
 988-1211/Domain: protein-tyrosine-phosphatase homology <PTP>  
 872/Active site: Cys (phosphocysteine intermediate) #status predicted  
 1163/Active site: Cys (phosphocysteine intermediate) #status predicted  
 1169/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.3%; Score 14; DB 2; Length 1231;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCAGVGRGTGVFI 370  
 |||||  
 1161 VHCAGVGRGTGVFI 1174

SULT 7  
 6493  
 uccocyte common antigen-related protein (LAR) - rat (fragment)  
 Alternate names: LAR receptor-linked tyrosine phosphatase  
 Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)  
 Species: Rattus norvegicus (Norway rat)  
 Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jan-2000  
 Accession: A56493; I55393  
 Zhang, J.S.; Longo, F.M.  
 Cell Biol. 128, 415-431, 1995  
 Title: LAR tyrosine phosphatase receptor: alternative splicing is preferential to the  
 Reference number: A56493; MUID:95146548; PMID:7844155  
 Accession: A56493  
 Status: translated from GB/EMBL/DBJ  
 Molecule type: mRNA  
 Residues: 1-1290 <RES>  
 Cross-references: EMBL:X83505; NID:g732918; PIDN:CAA58495.1; PID:g732919  
 Longo, F.M.; Martignetti, J.A.; Le Beau, J.M.; Zhang, J.S.; Barnes, J.P.; Brosius, J.  
 Biol. Chem. 268, 26503-26511, 1993  
 Title: Leukocyte common antigen-related receptor-linked tyrosine phosphatase. Regulation  
 Reference number: I55393; MUID:94075340; PMID:8253779  
 Accession: I55393  
 Status: translated from GB/EMBL/DBJ  
 Molecule type: mRNA  
 Residues: 831-1290 <RES>  
 Cross-references: EMBL:U00477; NID:g392565; PIDN:AA04306.1; PID:g392566  
 Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
 y  
 Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
 80-166/Domain: fibronectin type III repeat homology <3PR>  
 667-1290/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
 1047-1270/Domain: protein-tyrosine-phosphatase homology <PTP2>  
 931/Active site: Cys (phosphocysteine intermediate) #status predicted  
 937/Binding site: substrate phosphate (Arg) #status predicted  
 1222/Active site: Cys (phosphocysteine intermediate) #status predicted  
 1228/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.3%; Score 14; DB 2; Length 1290;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCAGVGRGTGVFI 370  
 |||||  
 1220 VHCAGVGRGTGVFI 1233

SULT 8  
 8758  
 otein-tyrosine-phosphatase (EC 3.1.3.48), receptor-linked form P1 precursor - rat  
 Species: Rattus norvegicus (Norway rat)  
 Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 Accession: A48758  
 Pan, M.G.; Rim, C.; Lu, K.P.; Florio, T.; Stork, P.J.S.  
 Biol. Chem. 268, 19284-19291, 1993  
 Title: Cloning and expression of two structurally distinct receptor-linked protein-tyr  
 Reference number: A48758; MUID:93374907; PMID:8396131

A:Accession: A48758  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1496 <PAN>  
 A:Cross-references: GB:I19180  
 A:Note: authors translated the codon TGC for residue 27 as Gly, GAG for residue 79 as Glu  
 as Phe  
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
 ocy  
 C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; transme  
 F:149-209/Domain: immunoglobulin homology <IMM1>  
 F:246-300/Domain: immunoglobulin homology <IMM2>  
 F:318-405/Domain: fibronectin type III repeat homology <FN3A>  
 F:411-504/Domain: fibronectin type III repeat homology <FN3B>  
 F:509-599/Domain: fibronectin type III repeat homology <FN3C>  
 F:600-684/Domain: fibronectin type III repeat homology <FN3H>  
 F:800-1496/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
 F:1256-1477/Domain: protein-tyrosine-phosphatase homology <PTP2>  
 F:1140/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1146/Binding site: substrate phosphate (Arg) #status predicted  
 F:1429/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1435/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.3%; Score 14; DB 1; Length 1496;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
 |||||  
 DB 1427 VHCAGVGRGTGVFI 1440

RESULT 9  
 I50212  
 Protein-tyrosine-phosphatase (EC 3.1.3.48) - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jan-2000  
 C:Accession: I50212  
 R:Stoker, A.W.  
 Mech. Dev. 46, 201-217, 1994  
 A:Title: Isoforms of a novel cell adhesion molecule-like protein tyrosine phosphatase are  
 A:Reference number: I50212; MUID:95001563; PMID:7918104  
 A:Accession: I50212  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1499 <STO>  
 A:Cross-references: GB:I32780; NID:g485746; PIDN:AA64460.1; PID:g485747  
 C:Genetics:  
 A:Gene: CRYPalpal  
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
 ocy  
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
 F:148-208/Domain: immunoglobulin homology <IMM1>  
 F:245-299/Domain: immunoglobulin homology <IMM2>  
 F:311-399/Domain: fibronectin type III repeat homology <3PR>  
 F:881-1499/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
 F:1257-1479/Domain: protein-tyrosine-phosphatase homology <PTP2>  
 F:1141/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1147/Binding site: substrate phosphate (Arg) #status predicted  
 F:1432/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1438/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.3%; Score 14; DB 2; Length 1499;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
 |||||  
 DB 1430 VHCAGVGRGTGVFI 1443

RESULT 10  
 I58148



Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCAGVGRGTGVFI 370  
|||||  
1793 VHCAGVGRGTGVFI 1806

SULT 13  
4689  
orcin-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precursor  
Alternate names: MPTP delta type B/C  
Contains: protein tyrosine phosphatase, receptor type delta, splice form C  
Species: Mus musculus (house mouse)  
Date: 25-Apr-1995 #sequence\_revision 19-May-1995 #text\_change 12-Feb-1999  
Accession: C54689; B54689  
Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.  
J. Cell. Biol. 13, 5513-5523, 1993  
Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in specialized  
Reference number: A54689; MUID:93360986; PMID:8355637  
Accession: C54689  
Status: preliminary  
Molecule type: mRNA  
Residues: 1-1894 <MIZ>  
Experimental source: brain; splice form B  
Note: sequence inconsistent with nucleotide translation  
Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBIPI:137487)  
Accession: B54689  
Status: preliminary  
Molecule type: mRNA  
Residues: 1-352 'H', 354-535 'S', 537-601, 1002-1894 <MIZ>  
Experimental source: brain; splice form C  
Note: sequence inconsistent with nucleotide translation  
Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBIPI:136530)  
Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
Y  
Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd

45-107/Domain: immunoglobulin homology <IMM1>  
245-299/Domain: immunoglobulin homology <IMM2>  
317-399/Domain: fibronectin type III repeat homology <FN3A>  
1278-1894/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP2>  
1536/Active site: Cys (phosphocysteine intermediate) #status predicted  
1542/Binding site: substrate phosphate (Arg) #status predicted  
1826/Active site: Cys (phosphocysteine intermediate) #status predicted  
1832/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.3%; Score 14; DB 2; Length 1894;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCAGVGRGTGVFI 370  
|||||  
1824 VHCAGVGRGTGVFI 1837

RESULT 14  
JHULK  
leukocyte antigen-related protein precursor - human  
Alternate names: leukocyte common antigen homolog  
Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)  
Species: Homo sapiens (man)  
Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 22-Jun-1999  
Accession: S03841; J00051  
Strulli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.  
Exp. Med. 168, 1523-1530, 1988  
Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region ho  
Reference number: J00051; MUID:89035978; PMID:2972792  
Accession: S03841  
Status: nucleic acid sequence not shown  
Molecule type: mRNA  
Residues: 1-1897 <STR>  
Cross-References: EMBL:Y00815; NID:g34266; PIDN:CAA68754.1; PID:g34267

C:Genetics:  
A:Gene: GDB:PTPRF; LAR  
A:Cross-References: GDB:120138; OMIM:179590  
A:Map position: 1p34-1p34  
A:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane I  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-1897/Product: leukocyte antigen-related protein #status predicted <MAT>  
F:17-1250/Domain: extracellular #status predicted <EXT>  
F:37-99/Domain: immunoglobulin homology <IMM1>  
F:139-199/Domain: immunoglobulin homology <IMM2>  
F:236-290/Domain: immunoglobulin homology <IMM3>  
F:308-390/Domain: fibronectin type III repeat homology <FN3A>  
F:403-489/Domain: fibronectin type III repeat homology <FN3B>  
F:501-583/Domain: fibronectin type III repeat homology <FN3C>  
F:596-685/Domain: fibronectin type III repeat homology <FN3D>  
F:698-798/Domain: fibronectin type III repeat homology #status atypical <FN3E>  
F:810-893/Domain: fibronectin type III repeat homology <FN3F>  
F:905-989/Domain: fibronectin type III repeat homology <FN3G>  
F:1001-1078/Domain: fibronectin type III repeat homology <FN3H>  
F:1251-1274/Domain: transmembrane #status predicted <TM>  
F:1275-1897/Domain: intracellular #status predicted <INT>  
F:1285-1897/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:1365-1897/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F:1654-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F:44-97, 146-197, 243-288/Disulfide bonds: #status predicted  
F:107, 240, 285, 711, 956/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:1538/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1544/Binding site: substrate phosphate (Arg) #status predicted  
F:1823/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1835/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.3%; Score 14; DB 1; Length 1897;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
|||||  
DB 1827 VHCAGVGRGTGVFI 1840

RESULT 15  
S46216  
leukocyte antigen-related protein precursor - rat  
Alternate names: leukocyte common antigen homolog  
N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S46216; S23252; A41032; A33154  
R:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.  
Biochem. J. 302, 39-47, 1994  
A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phos  
A:Reference number: S46216; MUID:94347119; PMID:8068021  
A:Accession: S46216  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-1898 <ZHA>  
A:Cross-References: EMBL:U111586; NID:9205132; PIDN:AAC37655.1; PID:g205133  
R:Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.  
Biochem. J. 284, 569-576, 1992  
A:Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by three  
A:Reference number: S23126; MUID:92287069; PMID:1599438  
A:Accession: S23126  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1361-1604, 1649-1898 <HAS>  
R:Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.  
J. Biol. Chem. 266, 19688-19696, 1991  
A:Title: Cloning, bacterial expression, purification, and characterization of the cytopla  
A:Reference number: A41032; MUID:92011772; PMID:1918076  
A:Accession: A41032  
A:Molecule type: mRNA



Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>  
Cross-references: GB:M60103; NID:Q205130; PIDN:AAA41510.1; PID:Q205131  
Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.  
Submitted to the Protein Sequence Database, December 1990  
Reference number: A33154  
Accession: A33154  
Molecule type: mRNA  
Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>  
Comment: Only the first of the two domains homologous with protein-tyrosine-phosphatase  
Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
Keywords: duplication; glycoprotein; phosphoprotein; phosphoric monoester hydrolase; 1-27/Domain: (or 1-26) signal sequence #status predicted <SIG>  
28-1898/Product: (or 27-1898) leukocyte antigen-related protein #status predicted <MAT>  
28-1251/Domain: (or 27-1251) extracellular #status predicted <EXT>  
47-109/Domain: immunoglobulin homology <IMM1>  
149-209/Domain: immunoglobulin homology <IMM2>  
246-300/Domain: immunoglobulin homology <IMM3>  
318-400/Domain: fibronectin type III repeat homology <FN3A>  
413-499/Domain: fibronectin type III repeat homology <FN3B>  
511-593/Domain: fibronectin type III repeat homology <FN3C>  
606-695/Domain: fibronectin type III repeat homology <FN3D>  
708-799/Domain: fibronectin type III repeat homology <FN3E>  
811-895/Domain: fibronectin type III repeat homology <FN3F>  
906-990/Domain: fibronectin type III repeat homology <FN3G>  
1002-1079/Domain: fibronectin type III repeat homology <FN3H>  
1252-1275/Domain: (or 1259-1275) transmembrane #status predicted <TM>  
1276-1898/Domain: intracellular #status predicted <INT>  
1286-1898/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
1366-1587/Domain: protein-tyrosine-phosphatase homology <PTP1>  
1658-1878/Domain: protein-tyrosine-phosphatase homology <PTP2>  
154-107156-207,253-298/Disulfide bonds: #status predicted  
117,250,295,721,957/Binding site: carbohydrate (Asn) (covalent) #status predicted  
1539/Active site: Cys (phosphocysteine intermediate) #status predicted  
1545/Binding site: substrate phosphate (Arg) #status predicted  
1830/Active site: Cys (phosphocysteine intermediate) #status predicted  
1836/Binding site: substrate phosphate (Arg) #status predicted  
Query Match 3.3%; Score 14; DB 2; Length 1898;  
Best Local Similarity 100.0%; Pred.No. 2.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 357 VHCAGVGRTGVFI 370  
||| ||||| |||||  
C 1828 VHCAGVGRTGVFI 1841

earch completed: June 16, 2004, 13:33:31  
ob time : 21 secs

sult No.	Score	Query Match	Length	DB	ID	Description	
1	15	3.5	1174	1	PTNL HUMAN	Q16825 homo sapien	
2	15	3.5	1175	1	PTNL RAT	Q62728 rattus norv	
3	15	3.5	1176	1	PTNL MOUSE	Q62136 mus musculu	
4	14	3.3	1897	1	PTPF HUMAN	P10586 homo sapien	
5	14	3.3	1912	1	PTPD HUMAN	P23468 homo sapien	
6	14	3.3	1948	1	PTNS HUMAN	Q13332 homo sapien	
7	12	2.8	1187	1	PTNE HUMAN	Q15678 homo sapien	
8	12	2.8	1189	1	PTNE MOUSE	Q62130 mus musculu	
9	12	2.8	1238	1	PTPJ MOUSE	Q64455 mus musculu	
10	12	2.8	1337	1	PTPJ HUMAN	Q12913 homo sapien	
11	12	2.8	1442	1	PTPG MOUSE	Q05909 mus musculu	
12	12	2.8	1445	1	PTPG HUMAN	P23470 homo sapien	
13	12	2.8	1462	1	PTPG_DROME	P16620 drosophila	
14	12	2.8	1705	1	PTPV MOUSE	P70289 mus musculu	
15	12	2.8	1711	1	PTPV RAT	Q04612 rattus norv	
16	11	2.6	335	1	PTP1 YEAST	P25044 saccharomyc	
17	11	2.6	521	1	PTP1_DICDI	P34137 dictyosteli	
18	11	2.6	550	1	PTP1_SCHPO	P27574 schizosacch	
19	11	2.6	699	1	PTPE MOUSE	P49446 mus musculu	
20	11	2.6	700	1	PTPE_HUMAN	P23469 homo sapien	
21	11	2.6	711	1	PTPE_SCHPO	P32586 schizosacch	
22	11	2.6	796	1	PTRA RAT	Q03348 rattus norv	
23	11	2.6	802	1	PTRA HUMAN	P18433 homo sapien	
24	11	2.6	829	1	PTRA MOUSE	P18052 mus musculu	
25	11	2.6	1152	1	CD45_MOUSE	Q06800 mus musculu	
26	11	2.6	1216	1	PTPO_HUMAN	Q16827 homo sapien	
27	11	2.6	1255	1	_CD45_RAT	P04157 rattus norv	
28	11	2.6	1301	1	PTP3_DROME	P35832 drosophila	
29	11	2.6	1304	1	CD45_HUMAN	P08575 homo sapien	
30	11	2.6	1422	1	PTPG CHICK	Q98936 gallus galli	
31	11	2.6	1997	1	PTPB HUMAN	P23467 homo sapien	
32	11	2.6	2029	1	LAR_DROME	P16621 drosophila	
33	11	2.6	2200	1	LAR_CAREEL	Q9bm38 caenorhabdi	

```

1 PROSITE: P500057; FERM_3; 1.
2 PROSITE: P500383; TYR_PHOSPHATASE_1; 1.
3 PROSITE: P500055; TYR_PHOSPHATASE_PTP; 1.
4 PROSITE: P500056; TYR_PHOSPHATASE_2; 1.
5 Structural protein; Cytoskeleton; Hydrolase.
6 DOMAIN 23 308 FERM.
7 DOMAIN 921 1174 PROTEIN-TYROSINE PHOSPHATASE.
8 ACT_SITE 1108 1108 PHOSPHOCYSTEINE INTERMEDIATE
9 (BY SIMILARITY).
10 DOMAIN 340 343 POLY-PRO.
11 DOMAIN 565 574 POLY-PRO.
12 DOMAIN 712 717 POLY-GLU.
13 SEQUENCE 1174 AA; 133287 MW; 5772D9B1A99B3FDA CRC64;
14
15 Query Match 3.5%; Score 15; DB 1; Length 1174;
16 Best Local Similarity 100.0%; Pred. No. 3.5e-07;
17 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
18
19 354 PLLVHCSAGVGTGV 368
20 1103 PLLVHCSAGVGTGV 1117
21
22 RESULT 2
23 PTNL_RAT STANDARD; PRT; 1175 AA.
24 Q62728; Q62732;
25 01-NOV-1997 (Rel. 35, Created)
26 01-NOV-1997 (Rel. 35, Last sequence update)
27 10-OCT-2003 (Rel. 42, Last annotation update)
28 Protein tyrosine phosphatase, non-receptor type 21 (EC 3.1.3.48)
29 (Protein-tyrosine phosphatase 2E).
30 PTPN21 OR PTP2E.
31 Rattus norvegicus (Rat).
32 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
33 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
34 NCBI_TaxID=10116;
35
36 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2E).
37 STRAIN=Sprague-Dawley;
38 MEDLINE=95104449; PubMed=7805871;
39 L'Abbe D., Banville D., Tong Y., Stocco R., Masson S., Ma S.,
40 Fantus G., Shen S.H.;
41 "Identification of a novel protein tyrosine phosphatase with sequence
42 homology to the cytoskeletal proteins of the band 4.1 family.";
43 FEBS Lett. 356:351-356(1994).
44
45 -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
46 tyrosine + phosphate.
47 -!- ALTERNATIVE PRODUCTS:
48 Event=Alternative splicing; Named isoforms=2;
49 Name=1;
50 IsoId=Q62728-1; Sequences=Displayed;
51 Name=2E;
52 IsoId=Q62728-2; Sequences=VSP 000498;
53 -!- TISSUE SPECIFICITY: Particularly abundantly in adrenal glands.
54 -!- SIMILARITY: Contains 1 PERM domain.
55 -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
56 Non-receptor class subfamily.
57
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59 between the Swiss Institute of Bioinformatics and the EMBL outstation -
60 the European Bioinformatics Institute. There are no restrictions on its
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64 or send an email to license@isb-sib.ch).
65
66 EMBL: U17971; AAA62153.1; -
67 EMBL: U18233; AAA62154.1; -
68 FIR: S51005; S51005.
69 HSP: Q06124; 2SHP.
70 InterPro: IPR000299; Band 4.1.
71 InterPro: IPR000387; TYR_phosphatase.
72
73 DR InterPro: IPR000242; Tyr_PP.
74 Pfam: PF00373; Band_41; 1.
75 Pfam: PF00102; Y_phosphatase; 1.
76 PRINTS: PR00935; BAND41.
77 PRINTS: PR00700; PRYPPHTASE.
78 SMART: SM00295; B41; 1.
79 SMART: SM00194; FIPC; 1.
80 PROSITE: P500660; FERM_1; 1.
81 PROSITE: P500661; FERM_2; 1.
82 PROSITE: P50057; FERM_3; 1.
83 PROSITE: P500383; TYR_PHOSPHATASE_1; 1.
84 PROSITE: P500055; TYR_PHOSPHATASE_PTP; 1.
85 PROSITE: P500056; TYR_PHOSPHATASE_2; 1.
86 Structural protein; Cytoskeleton; Hydrolase; Alternative splicing.
87 KW DOMAIN 23 308 FERM.
88 FT DOMAIN 922 1175 PROTEIN-TYROSINE PHOSPHATASE.
89 ACT_SITE 1109 1109 PHOSPHOCYSTEINE INTERMEDIATE
90 (BY SIMILARITY).
91 FT VARSPLIC 1 839 Missing (in isoform 2E).
92 FT /FTid=VSP_000498
93 SQ SEQUENCE 1175 AA; 133411 MW; 82A684F1C0F5ECF7 CRC64;
94
95 Query Match 3.5%; Score 15; DB 1; Length 1175;
96 Best Local Similarity 100.0%; Pred. No. 3.5e-07;
97 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
98
99 354 PLLVHCSAGVGTGV 368
100 1104 PLLVHCSAGVGTGV 1118
101
102 RESULT 3
103 PTNL_MOUSE STANDARD; PRT; 1176 AA.
104 Q62136;
105 01-NOV-1997 (Rel. 35, Created)
106 01-NOV-1997 (Rel. 35, Last sequence update)
107 10-OCT-2003 (Rel. 42, Last annotation update)
108 Protein tyrosine phosphatase, non-receptor type 21 (EC 3.1.3.48)
109 (Protein-tyrosine phosphatase PTP-RL10).
110 PTPN21.
111 Mus musculus (Mouse).
12 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
13 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
14 NCBI_TaxID=10090;
15 [1]
16 SEQUENCE FROM N.A.
17 STRAIN=C57BL/6; TISSUE=Liver;
18 MEDLINE=95140431; PubMed=7838337;
19 Higashitsuji H., Aril S., Furutani M., Imamura M., Kaneko Y.,
20 Takenawa J., Nakayama H., Fujita J.;
21 "Enhanced expression of multiple protein tyrosine phosphatases in the
22 regenerating mouse liver: isolation of PTP-RL10, a novel cytoplasmic-
23 type phosphatase with sequence homology to cytoskeletal protein
24 4.1.";
25 Oncogene 10:407-414(1995).
26 -!- FUNCTION: May be involved in the regulation of growth and
27 differentiation of liver cells.
28 -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
29 tyrosine + phosphate.
30 -!- TISSUE SPECIFICITY: Liver.
31 -!- SIMILARITY: Contains 1 PERM domain.
32 -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
33 Non-receptor class subfamily.
34
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36 between the Swiss Institute of Bioinformatics and the EMBL outstation -
37 the European Bioinformatics Institute. There are no restrictions on its
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39 modified and this statement is not removed. Usage by and for commercial
40 entities requires a license agreement (See http://www.isb-sib.ch/announce/
41 or send an email to license@isb-sib.ch).
42
43 EMBL: U17971; AAA62153.1; -
44 EMBL: U18233; AAA62154.1; -
45 FIR: S51005; S51005.
46 HSP: Q06124; 2SHP.
47 InterPro: IPR000299; Band 4.1.
48 InterPro: IPR000387; TYR_phosphatase.

```



Query Match 3.3%; Score 14; DB 1; Length 1897;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCAGVGRGTGVFI 370  
 1827 VHCAGVGRGTGVFI 1840

RESULT 5  
 \_PTPD HUMAN STANDARD; PRT; 1912 AA.  
 223458;  
 01-NOV-1991 (Rel. 20, Created)  
 01-OCT-1996 (Rel. 34, Last sequence update)  
 10-OCT-2003 (Rel. 42, Last annotation update)  
 3 Protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-  
 3 delta).  
 4 PTPRD.  
 5 Homo sapiens (Human).  
 6 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 7 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 8 NCBI\_TaxId=9606;  
 9 [1]  
 10 SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.  
 11 MEDLINE=95204468; PubMed=7896816;  
 12 Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;  
 13 "Molecular characterization of the human transmembrane protein-  
 14 tyrosine phosphatase delta. Evidence for tissue-specific expression of  
 15 alternative human transmembrane protein-tyrosine phosphatase delta  
 16 isoforms.";  
 17 J. Biol. Chem. 270:6722-6728 (1995).  
 18 [2]  
 19 SEQUENCE OF 390-1912 FROM N.A.  
 20 TISSUE=Placenta;  
 21 MEDLINE=91006018; PubMed=2170109;  
 22 Krueger N.X., Streuli M., Saito H.;  
 23 "Structural diversity and evolution of human receptor-like protein  
 24 tyrosine phosphatases.";  
 25 EMBO J. 9:3241-3252 (1990).  
 26 -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 27 tyrosine + phosphate.  
 28 -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 29 -!- ALTERNATIVE PRODUCTS:  
 30 Event=Alternative splicing; Named isoforms=3;  
 31 Comment=Additional isoforms seem to exist;  
 32 Name=1;  
 33 IsoId=P23468-1; Sequence=Displayed;  
 34 Name=2; Synonyms=kidney;  
 35 IsoId=P23468-2; Sequence=VSP\_005147, VSP\_005148, VSP\_005149;  
 36 Name=3; Synonyms=fetal brain;  
 37 IsoId=P23468-3; Sequence=VSP\_005150;  
 38 -!- PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN  
 39 FROM THE TRANSMEMBRANE SEGMENT.  
 40 -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.  
 41 -!- SIMILARITY: Contains 8 fibronectin type III domains.  
 42 -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
 43 -----  
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 45 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 47 use by non-profit institutions as long as its content is in no way  
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 50 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 51 -----  
 52 EMBL; L38929; AAC41749.1; --  
 53 EMBL; X54133; CAAB38068.1; --  
 54 PIR; A56178; A56178.  
 55 HSP; P18052; 1YFO.  
 56 Genew; HGNC:9668; PTPRD.  
 57 MIM; 601598; --  
 58 GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.  
 DR GO; GO:0005470; P:protein amino acid dephosphorylation; TAS.  
 DR GO; GO:0007185; P:transmembrane receptor protein tyrosine pho. . .; TAS.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003962; FNIII subd.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR InterPro; IPR000387; TYR phosphatase.  
 DR InterPro; IPR000242; TYR\_PP.  
 DR Pfam; PF00041; fn3; 8.  
 DR Pfam; PF00047; ig; 3.  
 DR Pfam; PF00102; I\_phosphatase; 2.  
 DR PRINTS; PRO0014; FNTYPEIII.  
 DR PRINTS; PRO0700; PTPYPTHTASE.  
 DR SMART; SM00060; PTPYPTHTASE.  
 DR SMART; SM00408; IGC2; 2.  
 DR SMART; SM00194; PTPC; 2.  
 DR PROSITE; PS50835; IG LIKE; 3.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
 DR Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Repeat;  
 KW Immunoglobulin domain; Alternative splicing.  
 KW SIGNAL 1 20  
 FT CHAIN 21 1912  
 FT DOMAIN 21 1265  
 FT TRANSMEM 1266 1390  
 FT DOMAIN 1291 1312  
 FT DOMAIN 24 114  
 FT DOMAIN 126 224  
 FT DOMAIN 236 318  
 FT DOMAIN 320 414  
 FT DOMAIN 417 513  
 FT DOMAIN 516 606  
 FT DOMAIN 609 708  
 FT DOMAIN 711 822  
 FT DOMAIN 825 916  
 FT DOMAIN 918 1017  
 FT DOMAIN 1020 1137  
 FT DOMAIN 1375 1618  
 FT DOMAIN 1619 1912  
 FT ACT\_SITE 1553 1553  
 FT ACT\_SITE 1844 1844  
 FT SITE 1175 1178  
 FT CARBOHYD 254 254  
 FT CARBOHYD 299 299  
 FT CARBOHYD 724 724  
 FT CARBOHYD 832 832  
 FT VARSPLIC 181 189  
 FT VARSPLIC 226 229  
 FT VARSPLIC 775 783  
 FT VARSPLIC 609 1137  
 FT MUTAGEN 1178 1178  
 FT SEQUENCE 1912 AA; 214759 MW; 3A88C8D32182E26 CRC64;  
 SQ  
 Query Match 3.3%; Score 14; DB 1; Length 1912;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
 DB 1842 VHCAGVGRGTGVFI 1855

RESULT 6  
 PTNS\_HUMAN

PTNS HUMAN STANDARD; PRT; 1948 AA.  
Q13332; Q15718; Q16341;  
10-OCT-2003 (Rel. 42, Created)  
10-OCT-2003 (Rel. 42, Last sequence update)  
10-OCT-2003 (Rel. 42, Last annotation update)  
Receptor-type protein-tyrosine phosphatase S precursor (EC 3.1.3.48)  
(R-PTP-S) (Protein-tyrosine phosphatase sigma) (R-PTP-sigma).  
PTPS.  
Homo sapiens (Human).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
TISSUE-Petal brain;  
MEDLINE=96102179; PubMed=8524829;  
Pulido R., Serra-Pages C., Tang M., Streuli M.;  
"The LAR/PTP delta/PPP sigma subfamily of transmembrane protein-  
tyrosine-phosphatases: multiple human LAR, PTP delta, and PTP sigma  
isoforms are expressed in a tissue-specific manner and associate with  
the LAR-interacting protein Lip.1.";  
Proc. Natl. Acad. Sci. U.S.A. 92:11686-11690(1995).  
[2]  
SEQUENCE FROM N.A.  
MEDLINE=9625038; PubMed=8992885;  
Endo N., Rutledge S.J., Opas E.E., Vogel R., Rodan G.A., Schmidt A.;  
"Human protein tyrosine phosphatase-sigma: alternative splicing and  
inhibition by bisphosphonates.";  
J. Bone Miner. Res. 11:535-543(1996).  
[3]  
SEQUENCE OF 1-126 FROM N.A.  
Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,  
Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,  
Phan H., Velasco M., Do L., Regala M., Terry A., Ganes J.,  
Danganan L., Brler A., Christensen M., Georgescu A., Avila J., Liu S.,  
Attix C., Andreise T., Trantham M., Amico-Keller G., Coefield J.,  
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,  
Arelano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,  
Olsen A.S., Carrano A.V.;  
"Sequence analysis of a 2.5 Mb region in 19p13.3.";  
Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.  
[4]  
SEQUENCE OF 1503-1589 FROM N.A.  
MEDLINE=92119637; PubMed=1370651;  
Adachi M., Sekiya M., Arimura Y., Takekawa M., Itoh F., Hinoda Y.,  
Imai K., Yachi A.;  
"Protein-tyrosine phosphatase expression in pre-B cell NALM-6.";  
Cancer Res. 52:737-740(1992).  
-1- FUNCTION: Interacts with LAR-interacting protein LIP.1.  
-1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
tyrosine + phosphate.  
-1- SUBCELLULAR LOCATION: Type I membrane protein.  
-1- ALTERNATIVE PRODUCTS:  
Event-Alternative splicing; Named isoforms=5;  
Comment-Additional isoforms seem to exist;  
Name=PTPS;  
IsoId=Q13332-1; Sequence=Displayed;  
Name=PTPS-MEA;  
IsoId=Q13332-2; Sequence=VSP\_050021;  
Name=PTPS-MEB;  
IsoId=Q13332-3; Sequence=VSP\_050022, VSP\_050026, VSP\_050027;  
Name=PTPS-MEC;  
IsoId=Q13332-4; Sequence=VSP\_050024;  
Name=PTPS-P4-7;  
IsoId=Q13332-5; Sequence=VSP\_050023, VSP\_050025;  
-1- TISSUE SPECIFICITY: Detected in all tissues tested except for  
placenta and liver.  
-1- SIMILARITY: BELONGS TO THE RECEPTOR CLASS OF THE PROTEIN-TYROSINE  
PHOSPHATASE FAMILY.  
-1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domain.  
-1- SIMILARITY: Contains 8 fibronectin type III domains.  
-1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
-----  
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CC DR EMBL; U5234; AAC50299.1; .  
CC DR EMBL; U40317; AAC50567.1; .  
CC DR EMBL; AC005790; AAC28232.1; .  
CC DR EMBL; S78080; AAB21146.2; .  
CC DR HSSP; P18052; 1YFO.  
CC DR Genew; HGNC:9681; PTPRS.  
CC DR MIM; 601576; .  
CC DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
CC DR GO; GO:0005001; P:transmembrane receptor protein tyrosine pho. .; TAS.  
CC InterPro; IPR008957; FN\_III-like.  
CC InterPro; IPR003961; FN\_III.  
CC InterPro; IPR003962; FNIII subd.  
CC InterPro; IPR007110; IG-like.  
CC InterPro; IPR003598; IG\_C2.  
CC InterPro; IPR00387; TYR phosphatase.  
CC InterPro; IPR000242; TYR\_PP.  
CC Pfam; PF00441; fn3; 8.  
CC Pfam; PF0047; IG; 3.  
CC Pfam; PF0102; Y\_Posphatase; 2.  
CC PRINTS; PR00014; FNTYPEIII.  
CC PRINTS; PR00700; PRTYPHPTASE.  
CC SMART; SM00060; FN3; 7.  
CC SMART; SM00408; IG\_C2; 3.  
CC SMART; SM00194; PTPC; 2.  
CC PROSITE; PS00835; IG\_LIKE; 3.  
CC PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
CC PROSITE; PS00556; TYR\_PHOSPHATASE\_2; 2.  
CC PROSITE; PS00555; TYR\_PHOSPHATASE\_PTP; 2.  
CC Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;  
Cell adhesion; Immunoglobulin domain; Alternative splicing; Repeat.  
FT SIGNAL 1 29  
FT CHAIN 30 1948  
FT RECEPTOR-TYPE PROTEIN-TYROSINE  
FT PHOSPHATASE S.  
FT EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 1283 1303  
FT CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 1304 1948  
FT IG-LIKE C2-TYPE 1.  
FT DOMAIN 33 123  
FT IG-LIKE C2-TYPE 2.  
FT DOMAIN 135 233  
FT IG-LIKE C2-TYPE 3.  
FT DOMAIN 245 327  
FT FIBRONECTIN TYPE-III 1.  
FT DOMAIN 329 423  
FT FIBRONECTIN TYPE-III 2.  
FT DOMAIN 426 522  
FT FIBRONECTIN TYPE-III 3.  
FT DOMAIN 525 615  
FT FIBRONECTIN TYPE-III 4.  
FT DOMAIN 618 717  
FT FIBRONECTIN TYPE-III 5.  
FT DOMAIN 720 831  
FT FIBRONECTIN TYPE-III 6.  
FT DOMAIN 834 926  
FT FIBRONECTIN TYPE-III 7.  
FT DOMAIN 928 1033  
FT FIBRONECTIN TYPE-III 8.  
FT DOMAIN 1036 1151  
FT PROTEIN-TYROSINE PHOSPHATASE 1.  
FT DOMAIN 1393 1648  
FT PROTEIN-TYROSINE PHOSPHATASE 2.  
FT DOMAIN 1680 1930  
FT POLY-PRO.  
FT DOMAIN 641 644  
FT POTENTIAL.  
FT DISULFID 54 107  
FT DISULFID 156 216  
FT DISULFID 266 311  
FT ACT\_SITE 1589 1589  
FT PHOSPHOCYSTEINE INTERMEDIATE (BY  
FT SIMILARITY).  
FT PHOSPHOCYSTEINE INTERMEDIATE (BY  
FT SIMILARITY).  
FT N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 263 263  
FT N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 308 308  
FT N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 733 733  
FT N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 940 940  
FT Missing (in isoform PTPS-MEA).  
FT VARSPLIC 190 138  
FT /FTID=VSP\_050021.  
FT Missing (in isoform PTPS-MEB).  
FT /FTID=VSP\_050022.  
FT VARSPLIC 236 239

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T VARSPLIC 617 1034 Missing (in isoform PTPS-F4-7).
T /FTId=VSP_050023.
T VARSPLIC 784 792 Missing (in isoform PTPS-MEC).
T /FTId=VSP_050024.
T VARSPLIC 1035 1035 V -> I (in isoform PTPS-F4-7).
T /FTId=VSP_050025.
T VARSPLIC 1350 1365 Missing (in isoform PTPS-MEB).
T /FTId=VSP_050026.
T VARSPLIC 1366 1366 S -> G (in isoform PTPS-MEB).
T /FTId=VSP_050027.
T CONFLICT 310 310 T -> HP (IN REF. 2).
T CONFLICT 428 429 SA -> RP (IN REF. 2).
T CONFLICT 742 745 LGPV -> RSPA (IN REF. 2).
T CONFLICT 765 773 GAGRGPPR -> RREARRGRS (IN REF. 2).
T CONFLICT 910 910 R -> P (IN REF. 2).
T CONFLICT 986 995 AAEPAENAV -> GRLGRARRTL (IN REF. 2).
T CONFLICT 1195 1196 TV -> SL (IN REF. 2).
T CONFLICT 1431 1431 F -> S (IN REF. 2).
T CONFLICT 1546 1546 E -> D (IN REF. 4).
T CONFLICT 1587 1587 V -> A (IN REF. 4).
T CONFLICT 1705 1705 N -> K (IN REF. 2).
Q SEQUENCE 1948 AA; 217080 MW; 7DC049EC03171136 CRC64;

Query Match 3.3%; Score 14; DB 1; Length 1948;
Best Local Similarity 100.0%; Pred. No. 6.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 357 VHCAGVGRGTGV 370
| | | | | | | | | |
b 1878 VHCAGVGRGTGV 1891

RESULT 7
TNE HUMAN STANDARD; PRT; 1187 AA.
D Q15678;
T 01-NOV-1997 (Rel. 35, Created)
T 01-NOV-1997 (Rel. 35, Last sequence update)
T 10-OCT-2003 (Rel. 42, Last annotation update)
E Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
E (Protein-tyrosine phosphatase pez).
N PTPN14 OR PEZ.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
P [1]
P SEQUENCE FROM N.A.
C TISSUE=Breast carcinoma;
C MEDLINE=95251727; PubMed=7733990;
A Smith A.L., Mitchell P.J., Shipley J., Gusterson B.A., Rogers M.V.,
A Crompton M.R.,
T "Pez: a novel human cDNA encoding protein tyrosine phosphatase- and
ezrin-like domains."
L Biochem. Biophys. Res. Commun. 209:959-965(1995).
C -/- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2O) = protein
tyrosine + phosphate.
C -/- TISSUE SPECIFICITY: Expressed in a variety of human tissues
including kidney, skeletal muscle, lung and placenta.
C -/- SIMILARITY: Contains 1 FERM domain.
C -/- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
-----
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or send an email to license@isb-sib.ch).
-----
R EMBL; X82676; CAA57993.1; --
R F01; J04155; J04155.

DR HSP: P29350; 1GWZ.
DR Genex: HGNC:9647; PTPN14.
DR MIM: 603155;
DR GO: GO:0004725; P:protein tyrosine phosphatase activity; TAS.
DR GO: GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro: IPR000299; Band 4.1.
DR InterPro: IPR000387; Tyr_PTPase.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00373; Band 41; 1.
DR Pfam: PF00102; Y_PTPase; 1.
DR PRINTS: PR00935; BAND41.
DR PRINTS: PR00700; PRTYPHTASE.
DR SMART: SM00295; B41; 1.
DR SMART: SM00194; PTEC; 1.
DR PROSITE: PS00660; FERM_1; 1.
DR PROSITE: PS00661; FERM_2; 1.
DR PROSITE: PS00557; FERM_3; 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS00555; TYR_PHOSPHATASE_PTP; 1.
DR PROSITE: PS00556; TYR_PHOSPHATASE_2; 1.
KW Structural protein; Cytoskeleton; Hydrolase.
FT DOMAIN 21 306 FERM.
FT DOMAIN 933 1187 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 1121 1121 PHOSPHOCYSTEINE INTERMEDIATE
(SY SIMILARITY).
FT DOMAIN 566 573 POLY-PRO.
FT DOMAIN 709 716 POLY-GLU.
SQ SEQUENCE 1187 AA; 135239 MW; 015760975E3574E3 CRC64;

Query Match 2.8%; Score 12; DB 1; Length 1187;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGV 368
| | | | | | | | | |
Db 1119 VHCAGVGRGTGV 1130

RESULT 8
PTNE MOUSE STANDARD; PRT; 1189 AA.
ID PTNE_MOUSE STANDARD; PRT; 1189 AA.
AC Q62130;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase PTP36).
DE PTPN14.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CB-17-SCID; TISSUE=Thymus;
RX MEDLINE=94354845; PubMed=8074693;
RA Sawada M., Ogata M., Fujino Y., Hamaoka T.;
RT "cDNA cloning of a novel protein tyrosine phosphatase with homology
to cytoskeletal protein 4.1 and its expression in T-lineage cells."
RL Biochem Biophys. Res. Commun. 203:479-484(1994).
CC -/- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF T CELL DEVELOPMENT.
CC -/- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2O) = protein
tyrosine + phosphate.
CC -/- TISSUE SPECIFICITY: Thymus; in cells of both hematopoietic and
non-hematopoietic origins.
CC -/- SIMILARITY: Contains 1 FERM domain.
CC -/- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
-----
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
R EMBL; X82676; CAA57993.1; --
R F01; J04155; J04155.
```

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EMBL; D31842; BAA06828.1; -;  
 PIR; JC2366; JC2366.  
 HSSP; Q06124; 28HP.  
 MGD; MGI:102467; Ptpn14.  
 InterPro; IPR000299; Band 4.1.  
 InterPro; IPR000387; Tyr\_Phosphatase.  
 InterPro; IPR000242; Tyr\_PP.  
 Pfam; PF00373; Band\_41; 1.  
 Pfam; PF00102; y\_phosphatase; 1.  
 PRINTS; PR00935; BAND41.  
 PRINTS; PR00700; PRTYPHPTASE.  
 SMART; SM00295; B41; 1.  
 SMART; SM00194; PTPC; 1.  
 PROSITE; PS00660; FERM\_1; 1.  
 PROSITE; PS00661; FERM\_2; 1.  
 PROSITE; PS00662; FERM\_3; 1.  
 PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 Structural protein; Cytoskeleton; Hydrolase.  
 DOMAIN 21 306 FERM  
 DOMAIN 935 1189 PROTEIN-TYROSINE PHOSPHATASE.  
 ACT\_SITE 1123 PHOSPHOCYSTEINE INTERMEDIATE  
 (BY SIMILARITY).  
 DOMAIN 566 573  
 DOMAIN 635 639 POLY-PRO.  
 DOMAIN 712 718 POLY-GLY.  
 SEQUENCE 1189 AA; 135030 MW; 2885B5F9C723303 CRC64;  
 Query Match 2.8%; Score 12; DB 1; Length 1189;  
 Best Local Similarity 100.0%; Pred. No. 0.00054;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 357 VHCAGVGTGCV 368  
 |||||  
 1121 VHCAGVGTGCV 1132  
 RESULT 9  
 PJ MOUSE  
 \_PTPJ MOUSE STANDARD; PRT; 1238 AA.  
 Q64455;  
 01-NOV-1997 (Rel. 35, Created)  
 01-NOV-1997 (Rel. 35, Last sequence update)  
 10-OCT-2003 (Rel. 42, Last annotation update)  
 Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)  
 (Hpp beta-like tyrosine phosphatase) (Protein-tyrosine phosphatase  
 receptor type J) (Susceptibility to colon cancer-1).  
 PTPRJ OR BYP OR SCCL.  
 Mus musculus (Mouse).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 STRAIN=MRL-LPR/LPR;  
 MEDLINE=96140699; PubMed=8549806;  
 Kuramochi S., Matsuda S., Matsuda Y., Saitoh T., Ohsugi M.,  
 Yamamoto T.;  
 "Molecular cloning and characterization of Byp, a murine  
 receptor-type tyrosine phosphatase similar to human DEP-1.";  
 PEBS Lett. 378:7-14(1996).  
 -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 tyrosine + phosphate.  
 -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 -!- TISSUE SPECIFICITY: Expressed in every tissue examined.  
 -!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.  
 -!- SIMILARITY: Contains 6 fibronectin type III domains.

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EMBL; D45212; BAA08146.1; -;  
 PIR; S68700; S68700.  
 HSSP; P18052; 1YFO.  
 MGD; MGI:104574; Ptpnj.  
 GO; GO:0007507; P:heart development; IMP.  
 GO; GO:0001570; P:vasculogenesis; IMP.  
 InterPro; IPR008957; FN III-like.  
 InterPro; IPR003961; FN III.  
 InterPro; IPR000387; Tyr\_Phosphatase.  
 InterPro; IPR00242; Tyr\_PP.  
 Pfam; PF00041; fn3; 6.  
 Pfam; PF00102; y\_phosphatase; 1.  
 PRINTS; PR00700; PRTYPHPTASE.  
 SMART; SM00060; FN3; 6.  
 SMART; SM00194; PTPC; 1.  
 PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 Signal; Glycoprotein; Transmembrane; Repeat; Hydrolase.  
 FT CHAIN 1 28 POTENTIAL.  
 FT DOMAIN 29 1238 PROTEIN-TYROSINE PHOSPHATASE ETA.  
 FT TRANSMEM 877 897 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 898 1238 POTENTIAL.  
 FT DOMAIN 40 112 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 121 260 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 268 348 FIBRONECTIN TYPE-III 2.  
 FT DOMAIN 356 434 FIBRONECTIN TYPE-III 3.  
 FT DOMAIN 442 518 FIBRONECTIN TYPE-III 4.  
 FT DOMAIN 529 608 FIBRONECTIN TYPE-III 5.  
 FT DOMAIN 966 1238 FIBRONECTIN TYPE-III 6.  
 FT ACT\_SITE 1140 PROTEIN-TYROSINE PHOSPHATASE.  
 FT CARBOHYD 62 PHOSPHOCYSTEINE INTERMEDIATE (BY  
 FT CARBOHYD 78 SIMILARITY).  
 FT CARBOHYD 85 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 90 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 110 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 114 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 145 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 164 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 173 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 182 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 207 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 244 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 253 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 267 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 278 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 313 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 333 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 379 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 403 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 437 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 452 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 488 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 506 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 538 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 572 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 576 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 662 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 668 N-LINKED (GLCNAC. . .) (POTENTIAL).





CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 501 501 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 525 525 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 536 536 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 582 582 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 666 666 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 761 761 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 772 772 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 784 784 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 790 790 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 824 824 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 910 910 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 937 937 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 VARIANT 214 214 R -> C (in colon cancer; somatic mutation).  
 VARIANT 276 276 /FTID=VAR\_015905.  
 Q -> P (in colon cancer; somatic mutation).  
 /FTID=VAR\_015906.  
 G -> D (IN REF. 1).  
 YNGKLEPLGYSR -> LOWEAGTSGLLP (IN REF. 2).  
 SEQUENCE 1337 AA; 145926 MW; E6752D521C4B6AFE CRC64;  
 Query Match 2.8%; Score 12; DB 1; Length 1337;  
 Best Local Similarity 100.0%; Pred. No. 0.00061;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 356 LVHCSAGVGRTG 367  
 1236 LVHCSAGVGRTG 1247  
 SULT 11  
 PG\_MOUSE  
 PTPG\_MOUSE STANDARD; PRT; 1442 AA.  
 Q05909;  
 01-FEB-1994 (Rel. 28, Created)  
 01-FEB-1994 (Rel. 28, Last sequence update)  
 10-OCT-2003 (Rel. 42, Last annotation update)  
 Protein-tyrosine phosphatase gamma precursor (EC 3.1.3.48) (R-PTP-gamma).  
 Mus musculus (Mouse).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 MEDLINE=93180796; PubMed=8382771;  
 Barnea G., Silvennoinen O., Shaanan B., Honegger A.M., Canoll P.D., D'Eustachio P., Morse B., Levy J.B., Laforgia S., Huebner K., Musacchio J.M., Sap J., Schlesinger J.;  
 "Identification of a carbonic anhydrase-like domain in the extracellular region of RPTP gamma defines a new subfamily of receptor tyrosine phosphatases." Mol. Cell. Biol. 13:1457-1506(1993).  
 -|- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.  
 -|- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
 -|- TISSUE SPECIFICITY: Detected in brain, lung, kidney, heart, liver,

CC skeletal muscle, spleen and testes. It is developmentally regulated in the brain.  
 CC -|- SIMILARITY: Contains 1 eukaryotic-type carbonic anhydrase domain.  
 CC -|- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
 CC -|- SIMILARITY: Contains 1 fibronectin type III domain.  
 CC  
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 CC  
 CC EMBL; L09562; AAA40022.1; -.  
 DR PIR; B48148; B48148.  
 DR HSSP; P18052; 1YFO.  
 DR MGD; MGI:97814; Ptpg.  
 DR InterPro; IPR001148; Euk\_COahnd.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR000387; TVR\_phosphatase.  
 DR InterPro; IPR000242; Tyr\_Pp.  
 DR Pfam; PF00194; carb\_anhydrase; 1.  
 DR Pfam; PF00041; fn3; 1.  
 DR Pfam; PF00102; Y\_phosphatase; 2.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR ProDom; PD000865; Euk\_COahnd; 1.  
 DR SMART; SM00060; FN3; 1.  
 DR SMART; SM00194; PTPC; 2.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Glycoprotein; Transmembrane; Hydrolase; Repeat; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 1442  
 FT DOMAIN 20 733  
 FT DOMAIN 734 759  
 FT TRANSMEM 760 1442  
 FT DOMAIN 56 322  
 FT DOMAIN 347 441  
 FT DOMAIN 866 1122  
 FT DOMAIN 1123 1442  
 FT ACT\_SITE 1057 1057  
 FT SITE 1348 1348  
 FT CARBOHYD 109 109  
 FT CARBOHYD 113 113  
 FT CARBOHYD 156 156  
 FT CARBOHYD 359 359  
 FT CARBOHYD 444 444  
 FT CARBOHYD 719 719  
 SQ SEQUENCE 1442 AA; 161242 MW; 5887715568FBECD8 CRC64;  
 Query Match 2.8%; Score 12; DB 1; Length 1442;  
 Best Local Similarity 100.0%; Pred. No. 0.00065;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 356 LVHCSAGVGRTG 367  
 DB 1054 LVHCSAGVGRTG 1065  
 RESULT 12  
 PTPG\_HUMAN  
 ID PTPG\_HUMAN STANDARD; PRT; 1445 AA.  
 AC P23470; Q15623;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase gamma precursor (EC 3.1.3.48) (R-PTP-gamma).  
 GN PTPRG.

Homo sapiens (Human);  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=93180796; PubMed=8382771;  
Barnea G., Silvennoinen O., Shaanan B., Honegger A.M., Canoll P.D.,  
D'Eustachio P., Morse B., Levy J.B., Laforgia S., Huebner K.,  
Musacchio J.M., Sap J., Schlessinger J.;  
"Identification of a carbonic anhydrase-like domain in the  
extracellular region of RPTP gamma defines a new subfamily of  
receptor tyrosine phosphatases.";  
Mol. Cell. Biol. 13:1497-1506(1993).  
[2]  
SEQUENCE FROM N.A.  
MEDLINE=96429999; PubMed=8933149;  
Kastury K., Ohta M., Lasota J., Moir D., Dorman T., Laforgia S.,  
Druck T., Huebner K.;  
"Structure of the human receptor tyrosine phosphatase gamma gene  
(PTPRG) and relation to the familial RCC t(3;6) chromosome  
translocation.";  
Genomics 32:225-235(1996).  
[3]  
SEQUENCE OF 836-1445 FROM N.A.  
TISSUE=Placenta;  
MEDLINE=91006018; PubMed=2170109;  
Krueger N.X., Streuli M., Saito H.;  
"Structural diversity and evolution of human receptor-like protein  
tyrosine phosphatases.";  
EMBO J. 9:3241-3252(1990).  
[4]  
SEQUENCE OF 874-1118 AND 1175-1409 FROM N.A.  
TISSUE=Brain;  
MEDLINE=90384936; PubMed=2169617;  
Kaplan R., Morse B., Huebner K., Croce C., Howk R., Ravera M.,  
Ricca G., Jaye M., Schlessinger J.;  
"Cloning of three human tyrosine phosphatases reveals a multigene  
family of receptor-linked protein-tyrosine-phosphatases expressed in  
brain.";  
Proc. Natl. Acad. Sci. U.S.A. 87:7000-7004(1990).  
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
tyrosine + phosphate.  
-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
-!- TISSUE SPECIFICITY: Found in a variety of tissues. It is  
developmentally regulated in the brain (By similarity).  
-!- SIMILARITY: Contains 1 eukaryotic-type carbonic anhydrase domain.  
-!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
-!- SIMILARITY: Contains 1 fibronectin type III domain.  
-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; L09247; AAC50224.1; -;  
EMBL; U46116; AAC50439.1; -;  
EMBL; U46089; AAC50439.1; JOINED.  
EMBL; U46090; AAC50439.1; JOINED.  
EMBL; U46091; AAC50439.1; JOINED.  
EMBL; U46092; AAC50439.1; JOINED.  
EMBL; U46093; AAC50439.1; JOINED.  
EMBL; U46094; AAC50439.1; JOINED.  
EMBL; U46095; AAC50439.1; JOINED.  
EMBL; U46096; AAC50439.1; JOINED.  
EMBL; U46097; AAC50439.1; JOINED.  
EMBL; U46098; AAC50439.1; JOINED.  
EMBL; U46099; AAC50439.1; JOINED.  
EMBL; U46100; AAC50439.1; JOINED.  
EMBL; U46101; AAC50439.1; JOINED.

DR EMBL; U46102; AAC50439.1; JOINED.  
DR EMBL; U46103; AAC50439.1; JOINED.  
DR EMBL; U46104; AAC50439.1; JOINED.  
DR EMBL; U46105; AAC50439.1; JOINED.  
DR EMBL; U46106; AAC50439.1; JOINED.  
DR EMBL; U46107; AAC50439.1; JOINED.  
DR EMBL; U46108; AAC50439.1; JOINED.  
DR EMBL; U46109; AAC50439.1; JOINED.  
DR EMBL; U46110; AAC50439.1; JOINED.  
DR EMBL; U46111; AAC50439.1; JOINED.  
DR EMBL; U46112; AAC50439.1; JOINED.  
DR EMBL; U46113; AAC50439.1; JOINED.  
DR EMBL; U46114; AAC50439.1; JOINED.  
DR EMBL; U46115; AAC50439.1; JOINED.  
DR EMBL; X54132; CAA38067.1; -;  
DR PIR; A48148; A48148.  
DR HSSP; P18052; LYFO.  
DR Genew; HGNC:9671; PTPRG.  
DR MIM; 176886; -;  
DR GO; GO:0005887; C: integral to plasma membrane; TAS.  
DR GO; GO:0005001; P: transmembrane receptor protein tyrosine pho. . . ; TAS.  
DR GO; GO:0007169; P: transmembrane receptor protein tyrosine kin. . . ; TAS.  
DR InterPro; IPR001148; Euk Coanhd.  
DR InterPro; IPR003957; FN III-like.  
DR InterPro; IPR003361; FN III.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR000242; Tyr\_Pp.  
DR Pfam; PF00194; carb\_anhydase; 1.  
DR Pfam; PF00041; fn3; 1.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR PRINTS; PR00700; PRTYPHPTASE.  
DR ProDom; PD000865; Euk Coanhd; 1.  
DR SMART; SM00060; FN3; 1.  
DR SMART; SM00194; FTPC; 2.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE 1; 1.  
DR PROSITE; PS00056; TYR\_PHOSPHATASE 2; 2.  
DR PROSITE; PS00055; TYR\_PHOSPHATASE PTP; 2.  
KW Glycoprotein; Transmembrane; Hydrolase; Phosphorylation; Repeat;  
KW Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 1445 PROTEIN-TYROSINE PHOSPHATASE GAMMA.  
FT DOMAIN 20 736 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 737 762 POTENTIAL.  
FT DOMAIN 763 1445 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 56 322 CARBONIC-ANHYDRASE LIKE.  
FT DOMAIN 347 441 FIBRONECTIN TYPE-III.  
FT DOMAIN 869 1125 PROTEIN-TYROSINE PHOSPHATASE 1.  
FT DOMAIN 1126 1445 PROTEIN-TYROSINE PHOSPHATASE 2.  
FT ACT\_SITE 1060 1060 PHOSPHOCYSTEINE INTERMEDIATE (BY  
SIMILARITY).  
FT SITE 1351 1351 ANCESTRAL ACTIVE SITE.  
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 112 113 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 619 619 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 631 631 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 722 722 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 80 80 S -> G (IN REF. 2).  
FT CONFLICT 92 92 Y -> H (IN REF. 2).  
FT CONFLICT 549 549 A -> V (IN REF. 2).  
FT CONFLICT 756 756 I -> T (IN REF. 2).  
FT CONFLICT 1407 1407 R -> M (IN REF. 3).  
SQ SEQUENCE 1445 AA; 162058 MW; 350FB90DC94E808D CRC64;

Query Match 2.8%; Score 12; DB 1; Length 1445;

Best Local Similarity 100.0%; Pred. No. 0.00065; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0;

QY 356 LVHCSAGVGRTG 367

DB 1057 LVHCSAGVGRTG 1068

SULT 13  
P6 DROME STANDARD; PRT; 1462 AA.  
P16620;  
01-AUG-1990 (Rel. 15, Created)  
01-AUG-1990 (Rel. 15, Last sequence update)  
10-OCT-2003 (Rel. 42, Last annotation update)  
Protein-tyrosine phosphatase DPTP precursor (EC 3.1.3.48) (Protein-tyrosine-phosphate phosphohydrolase).  
PTP69D OR DPTP.  
Drosophila melanogaster (Fruit fly).  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
NCBI\_TaxID=7227;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=90046860; PubMed=2554325;  
Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;  
"A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila.";  
Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).  
-!- FUNCTION: It is possible that DPTP is a cell adhesion receptor.  
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.  
-!- SUBCELLULAR LOCATION: Type I membrane protein.  
-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
-!- SIMILARITY: Contains 2 fibronectin type III domains.  
-!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
-----  
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EMBL; M27699; AAA28842.1; -;  
PIR; B36182; B36182.  
HSSP; P18052; 1VFO.  
FlyBase: FBgn014007; Ptp69D.  
GO; GO:0004725; P:protein tyrosine phosphatase activity; IDA.  
GO; GO:0007435; P:defasciculation of motor neuron; IGI.  
GO; GO:0008045; P:motor axon guidance; IGI.  
GO; GO:0006470; P:protein amino acid dephosphorylation; IDA.  
InterPro; IPR008957; FN\_III-like.  
InterPro; IPR003961; FN\_III.  
InterPro; IPR007110; IG-like.  
InterPro; IPR003598; IG\_c2.  
InterPro; IPR003387; Tyr\_phosphatase.  
InterPro; IPR000242; Tyr\_PP.  
Pfam; PF00041; fn3; 3.  
Pfam; PF00047; ig; 2.  
Pfam; PF00102; Y\_phosphatase; 2.  
PRINTS; PR00700; PRTYPHPTASE.  
SMART; SM00060; FN3; 3.  
SMART; SM00408; IGc2; 1.  
SMART; SM00194; PTPc; 2.  
PROSITE; PS50835; IG LIKE; 2.  
PROSITE; PS00383; TYR\_PHOSPHATASE 1; 2.  
PROSITE; PS50056; TYR\_PHOSPHATASE 2; 2.  
PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;  
Cell adhesion; Immunoglobulin domain; Repeat.  
SIGNAL  
CHAIN 1 23  
RP 24 1462 PROTEIN-TYROSINE PHOSPHATASE DPTP.  
DOMAIN 24 805 EXTRACELLULAR (POTENTIAL).  
TRANSMEM 806 823 POTENTIAL.  
DOMAIN 824 1462 CYTOSOLASMIC (POTENTIAL).  
DOMAIN 24 125 IG-LIKE C2-TYPE 1.

FT DOMAIN 131 230 IG-LIKE C2-TYPE 2.  
FT DOMAIN 332 437 FIBRONECTIN TYPE-III 1.  
FT DOMAIN 438 538 FIBRONECTIN TYPE-III 2.  
FT DOMAIN 912 1165 PROTEIN-TYROSINE PHOSPHATASE 1.  
FT DOMAIN 1208 1459 PROTEIN-TYROSINE PHOSPHATASE 2.  
FT ACT\_SITE 1097 1097 PHOSPHOCYSTEINE INTERMEDIATE (BY  
SIMILARITY).  
FT ACT\_SITE 1391 1391 PHOSPHOCYSTEINE INTERMEDIATE (BY  
SIMILARITY).  
FT DISULFID 45 112 POTENTIAL.  
FT DISULFID 154 214 POTENTIAL.  
FT CARBOHYD 58 40 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 429 429 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 516 516 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 701 701 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 755 755 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 1462 AA; 167411 MW; P8091D69B88230EB CRC64;  
Query Match 2.8%; Score 12; DB 1; Length 1462;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 356 LVHCSAGVGRTG 367  
DB 1094 LVHCSAGVGRTG 1105  
RESULT 14  
PTPV MOUSE  
ID PTPV MOUSE STANDARD; PRT; 1705 AA.  
AC P70289;  
DC 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Receptor-type protein-tyrosine phosphatase V precursor (EC 3.1.3.48)  
DE DE (Embryonic stem cell protein-tyrosine phosphatase)  
DE phosphatase).  
GN PTPRV OR ESP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryonic stem cells;  
RX MEDLINE=97109513; PubMed=8951793;  
RA Lee K., Nichols J., Smith A.;  
RT "Identification of a developmentally regulated protein tyrosine  
phosphatase in embryonic stem cells that is a marker of  
pluripotential epiblast and early mesoderm.";  
RL Mech. Dev. 59:153-164(1996).  
RN [2]  
RP ERRATUM.  
RA Lee K., Nichols J., Smith A.;  
RL Mech. Dev. 61:213-215(1996).  
CC -!- FUNCTION: May play a role in the maintenance of pluripotency.  
CC Down-regulated during differentiation.





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(protein - protein search, using sw model

on: June 16, 2004, 13:28:47 ; Search time 45 Seconds  
(without alignments)

2986.906 Million cell updates/sec

file: US-09-095-478A-5

Effect score: 426

Sequence: 1 MSSPRKVRGKTGRNDDEEG.....QYQFCEIVLEVLQNLLALY 426

oring table:

Gapop 60.0 , Gapext 60.0

arched: 1017041 seqs, 315518202 residues

ord size : 0

tal number of hits satisfying chosen parameters: 1017041

nimum DB seq length: 0

ximum DB seq length: 2000000000

st-processing: Listing first 45 summaries

tabase :

SPTREMBL 25:\*

1: sp archea:\*

2: sp bacteria:\*

3: sp fungi:\*

4: sp human:\*

5: sp invertebrate:\*

6: sp mammal:\*

7: sp mhc:\*

8: sp organelle:\*

9: sp phage:\*

10: sp plant:\*

11: sp rodent:\*

12: sp virus:\*

13: sp vertebrate:\*

14: sp unclassified:\*

15: sp rvirus:\*

16: sp bacteriap:\*

17: sp archaep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

sult No.	Score	Query Match	Length	DB ID	Description
1	426	100.0	426	11	O55082 mus muscu
2	19	4.5	398	4	Q9Y406 homo sapien
3	15	3.5	336	11	Q9QWQ7 mus muscu
4	15	3.5	446	5	Q9Y1X4 ephydattia f
5	15	3.5	758	11	Q7TNG1 mus muscu
6	15	3.5	1024	4	O8WX29 homo sapien
7	14	3.3	24	11	O88571 mus spretus
8	14	3.3	24	11	O88570 mus muscu
9	14	3.3	79	11	O8CC23 mus muscu
10	14	3.3	93	11	O8CC54 mus muscu
11	14	3.3	134	4	Q9UMZ3 homo sapien
12	14	3.3	183	5	Q9Y1X3 ephydattia f
13	14	3.3	192	11	O8C922 mus muscu
14	14	3.3	460	11	Q62917 rattus norv
15	14	3.3	468	13	Q91BA5 potamotrygo
16	14	3.3	468	13	Q91BA2 potamotrygo

Q91BA0 potamotrygo  
Q9Y15 brachydanio  
Q64696 mus muscu  
Q91A18 xenopus lae  
Q8R169 mus muscu  
Q9YJ4 brachydanio  
Q723X4 homo sapien  
Q17024 anophelies g  
Q8VBV0 mus muscu  
Q75870 homo sapien  
Q90815 gallus gall  
Q9QWQ0 rattus sp.  
Q7T17 mus muscu  
Q9UM81 homo sapien  
Q91A30 xenopus lae  
Q64605 rattus norv  
Q9QW67 rattus sp.  
Q64487 mus muscu  
Q91A11 xenopus lae  
Q86WS0 homo sapien  
Q9EQ17 mus muscu  
Q64604 r protein-t  
Q64699 mus muscu  
Q44328 hirudo medi  
Q88488 rattus norv  
Q9N111 branchiosto  
Q9N108 eptatetus  
Q9J136 mus muscu  
O02048 caenorhabdi

# ALIGNMENTS

## RESULT 1

O55082 ID O55082 PRELIMINARY; PRT; 426 AA.  
AC O55082  
DT 01-JUN-1998 (TREMREL. 06, Created)  
DT 01-JUN-1998 (TREMREL. 06, Last sequence update)  
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)  
DE Protein-tyrosine-phosphatase (EC 3.1.3.48).  
GN PTPN20.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RX MEDLINE=98070510; PubMed=9407093;  
RA Ohagi M., Kuramochi S., Matsuda S., Yamamoto T.;  
RT "Molecular cloning and characterization of a novel cytoplasmic  
RT protein-tyrosine phosphatase that is specifically expressed in  
RT spermatocytes.";  
RL J. Biol. Chem. 272:33092-33099(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
DR EMBL; D64141; BAA23761.1; --  
DR EMBL; AK029493; BAC26476.1; --  
DR HSSP; Q06124; 2SHP.  
DR Q9UMZ3 homo sapien  
DR MGD; MGI:1196295; Ptpn20.  
DR GO; GO:0016787; F:Hydrolase activity; IEA.  
DR GO; GO:0004727; F:Phosphorylated protein tyrosine phosphatase act. .; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000387; TVR\_phosphatase.

December

```
InterPro; IPR000242; Tyr_PP.  
Pfam; PF00102; Y_phosphatase; 1.  
PRINTS; PR00700; PRTVPHPTASE.  
SMART; SM00194; PTPC; 1.  
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.  
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.  
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.  
Hypothetical protein; Hydrolase.  
NON_TER 1  
SQ SEQUENCE 426 AA; 49118 MW; 2B35FB13379502P4 CRC64;  
  
Query Match 100.0%; Score 426; DB 11; Length 426;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 MSSPRKVGKGTGRNDDEEGNSGNLRLNSLPSSSQMTPTKIFGNKXNSNVKPSHLL 60  
1 MSSPRKVGKGTGRNDDEEGNSGNLRLNSLPSSSQMTPTKIFGNKXNSNVKPSHLL 60  
  
61 SFSDKYELVYPEPLESDTETVWDVSDRLNRNWNDSVETAGPSKTVSPVLGSSRLSK 120  
61 SFSDKYELVYPEPLESDTETVWDVSDRLNRNWNDSVETAGPSKTVSPVLGSSRLSK 120  
  
121 DTETSVSEKLTQLAQIRPLIFNSARSAMRDCLNTLQKKEELDIIREFLEQLQMTLPDD 180  
121 DTETSVSEKLTQLAQIRPLIFNSARSAMRDCLNTLQKKEELDIIREFLEQLQMTLPDD 180  
  
181 FNSGNTLQNRKRYRDLIPDSTRVPLGKNKDYINASYIRIYNHBEYFYIATQGPLPE 240  
181 FNSGNTLQNRKRYRDLIPDSTRVPLGKNKDYINASYIRIYNHBEYFYIATQGPLPE 240  
  
241 TIEDFWQVLENNCNVIANITRBEICGVKICYSYWPISLKEPLEFHFVLETFHTVQY 300  
241 TIEDFWQVLENNCNVIANITRBEICGVKICYSYWPISLKEPLEFHFVLETFHTVQY 300  
  
301 FTVRVFQIVKSTGSKQCCKHLOFTKPDHGTPASADFFIKYIVYVKSHITGELLVHCS 360  
301 FTVRVFQIVKSTGSKQCCKHLOFTKPDHGTPASADFFIKYIVYVKSHITGELLVHCS 360  
  
361 AGVGRTGVFCVDVVFSIAEKNGYFSDIMNIVTQMKQRCGMIQTKEQYQCYEIVLEVLQ 420  
361 AGVGRTGVFCVDVVFSIAEKNGYFSDIMNIVTQMKQRCGMIQTKEQYQCYEIVLEVLQ 420  
  
421 NLLALY 426  
421 NLLALY 426  
  
RESULT 2  
QY406 PRELIMINARY; PRT; 398 AA.  
QY406; 01-NOV-1999 (TREMBlrel. 12, Created)  
QY406; 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
QY406; 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
E Hypothetical protein (Fragment).  
S Homo sapiens (Human).  
S Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
S Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
X NCBI_TaxID=9606;  
X [1]  
X SEQUENCE FROM N.A.  
X TISSUE=Kidney;  
X Ansoorge W., Wirkner U., Mewes H.W., Gassenhuber J., Wiemann S.;  
X Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
L EMBL; AL050040; CAB43248.1; --  
R PIR; T08716; T08716.  
R HSSP; Q06124; 2SHP.  
R GO; GO:0016787; F:hydrolase activity; IEA.  
R GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
R GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
R InterPro; IPR000387; TYR_phosphatase.  
R InterPro; IPR000242; Tyr_PP.
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Pfam; PF00102; Y_phosphatase; 1.  
PRINTS; PR00700; PRTVPHPTASE.  
SMART; SM00194; PTPC; 1.  
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.  
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.  
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.  
Hypothetical protein; Hydrolase.  
NON_TER 1  
SQ SEQUENCE 398 AA; 45690 MW; 857AAD03747870A2 CRC64;  
  
Query Match 4.5%; Score 19; DB 4; Length 398;  
Best Local Similarity 100.0%; Pred. No. 2.9e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 192 KNYRDILPYDSTRVPLGK 210  
Db 164 KNYRDILPYDSTRVPLGK 182  
  
RESULT 3  
Q9QWQ7 PRELIMINARY; PRT; 336 AA.  
Q9QWQ7; 01-MAY-2000 (TREMBlrel. 13, Created)  
Q9QWQ7; 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
Q9QWQ7; 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
D3 PTP-RL10b.  
D3 PTPN21.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
OX [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-C57-BL/6; TISSUE=Testis;  
RA Nishiyama H., Higashitsuji H., Fujita J.;  
RT Expression of mouse PTP-RL10 isoforms in testis.;  
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; D83072; BAA19740.1; --  
DR HSSP; P29350; IGWZ.  
DR MGD; MGI:1344406; Ptpn21.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000387; TYR_phosphatase.  
DR InterPro; IPR00242; Tyr_PP.  
DR Pfam; PF00102; Y_phosphatase; 1.  
DR PRINTS; PR00700; PRTVPHPTASE.  
DR SMART; SM00194; PTPC; 1.  
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.  
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.  
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.  
KW Hydrolase.  
SQ SEQUENCE 336 AA; 38503 MW; 679B683660C39FFD CRC64;  
  
Query Match 3.5%; Score 15; DB 11; Length 336;  
Best Local Similarity 100.0%; Pred. No. 5.1e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 354 PLLVHCASAGVGRGTGV 368  
Db 265 PLLVHCASAGVGRGTGV 279  
  
RESULT 4  
Q9YIX4 PRELIMINARY; PRT; 446 AA.  
Q9YIX4; 01-NOV-1999 (TREMBlrel. 12, Created)  
Q9YIX4; 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
Q9YIX4; 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE SPTP25 (Fragment).  
OS Ephydratia fluviatilis.
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Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;  
Haploclerida; Spongillidae; Ephydatia.  
NCBI\_TaxID=31330;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=92246376; PubMed=10229569;  
Ono K., Suga H., Iwabe N., Kuma K., Miyata T.;  
"Multiple protein tyrosine phosphatases in sponges and explosive gene  
duplication in the early evolution of animals before the parazoan-  
eumetazoan split.";  
J. Mol. Evol. 48:654-662(1999).  
EMBL; AB019127; BAAR2560.1; -.  
HSSP; P18052; 1VPO.  
GO; GO:0016787; P:hydrolase activity; IEA.  
GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
InterPro; IPR000387; Tyr\_PP.  
Pfam; PF00102; Y\_phosphatase; 2.  
PRINTS; PR00700; PTPHPTASE.  
SMART; SM00194; PTPC; 2.  
PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
Hydrolase.  
NON TER 1 1  
SEQUENCE 446 AA; 50365 MW; 9B5B8AF6168DF7C CRC64;  
Query Match 3.5%; Score 15; DB 5; Length 446;  
Best Local Similarity 100.0%; Pred. No. 6.6e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
353 GPLLVHCSAGVGRGTG 367  
|||||  
1.02 GPLLVHCSAGVGRGTG 116  
SULT 5  
TWG1  
Q7TMG1 PRELIMINARY; PRT; 758 AA.  
Q7TMG1;  
01-OCT-2003 (TrEMBLrel. 25, Created)  
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
Protein tyrosine phosphatase, non-receptor type 21 (Fragment).  
Mus musculus (Mouse).  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=CZECH II; TISSUE=Breast tumor;  
MEDLINE=22388257; PubMed=12477932;  
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Parner A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]  
SEQUENCE FROM N.A.  
RA STRAIN=CZECH II; TISSUE=Breast tumor;  
RA Strausberg R.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC055942; AAHS5942.1; -.  
KW Receptor.  
FT NON TER 1 1  
SEQUENCE 758 AA; 85514 MW; 6C3CAB40C026BD37 CRC64;  
Query Match 3.5%; Score 15; DB 11; Length 758;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 354 PLLVHCSAGVGRGTG 368  
|||||  
DB 697 PLLVHCSAGVGRGTG 701  
RESULT 6  
Q8WX29 PRELIMINARY; PRT; 1024 AA.  
AC Q8WX29;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE DJ1175915.2 (Protein tyrosine phosphatase, non-receptor type 21)  
DE (Fragment).  
GN PTPN21.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Horden P.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL353786; CAD19000.1; -.  
DR GO; GO:0005856; C:cytoskeleton; IEA.  
DR GO; GO:0016787; P:hydrolase activity; IEA.  
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0004872; P:receptor activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000299; Band 4.1.  
DR InterPro; IPR000387; Tyr\_phosphatase.  
DR InterPro; IPR00242; Tyr\_PP.  
DR Pfam; PF00102; Y\_phosphatase; 1.  
DR PRINTS; PR00700; PTPHPTASE.  
DR SMART; SM00194; PTPC; 1.  
DR PROSITE; PS00661; FERM\_2; 1.  
DR PROSITE; PS00057; FERM\_3; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
KW Hydrolase; Receptor.  
FT NON TER 1 1  
SEQUENCE 1024 AA; 115763 MW; C702F90D6AF38EAB CRC64;  
Query Match 3.5%; Score 15; DB 4; Length 1024;  
Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 354 PLLVHCSAGVGRGTG 368  
|||||  
DB 953 PLLVHCSAGVGRGTG 967  
RESULT 7  
O88571 PRELIMINARY; PRT; 24 AA.  
ID O88571;  
AC O88571;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

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01-JUN-2003 (TRENBLrel. 24, Last annotation update)
Protein tyrosine phosphatase rPTP-GW1 (Fragment).
PTPRQ.
Mus spretus (Western wild mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10096;
[1]
SEQUENCE FROM N.A.
MEDLINE=98395110; PubMed=9727007;
Wright M.B., Hugo C., Seifert R., Disteche C.M., Bowen-Pope D.F.;
"Proliferating and migrating mesangial cells responding to injury
express a novel receptor protein-tyrosine phosphatase in experimental
mesangial proliferative glomerulonephritis.";
J. Biol. Chem. 273:23929-23937(1998).
EMBL; AF073998; AAC34823.1; -.
MGD; MGI:1096349; PTPRQ.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004721; P:protein phosphatase activity; IEA.
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
InterPro; IPR000387; TYR_PHOSPHATASE_1; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
Hydrolase.
NON_TER 1 1
NON_TER 24 24
SEQUENCE 24 AA; 2483 MW; 781A5FBF2BC2E2B CRC64;

Query Match 3.3%; Score 14; DB 11; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCAGVGTGVFI 370
|||||
10 VHCAGVGTGVFI 23

SULT 8
18570
088570 PRELIMINARY; PRT; 24 AA.
088570;
01-NOV-1998 (TRENBLrel. 08, Created)
01-NOV-1998 (TRENBLrel. 08, Last sequence update)
01-JUN-2003 (TRENBLrel. 24, Last annotation update)
Protein tyrosine phosphatase rPTP-GW1 (Fragment).
PTPRQ.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=98395110; PubMed=9727007;
Wright M.B., Hugo C., Seifert R., Disteche C.M., Bowen-Pope D.F.;
"Proliferating and migrating mesangial cells responding to injury
express a novel receptor protein-tyrosine phosphatase in experimental
mesangial proliferative glomerulonephritis.";
J. Biol. Chem. 273:23929-23937(1998).
EMBL; AF073998; AAC34822.1; -.
MGD; MGI:1096349; PTPRQ.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004721; P:protein phosphatase activity; IEA.
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
InterPro; IPR000387; TYR_PHOSPHATASE_1; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
Hydrolase.
NON_TER 1 1
NON_TER 24 24
SEQUENCE 24 AA; 2483 MW; 781A5FBF2BC2E2B CRC64;

Query Match 3.3%; Score 14; DB 11; Length 24;
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Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGTGVFI 370
|||||
Db 10 VHCAGVGTGVFI 23

RESULT 9
Q8CC23 PRELIMINARY; PRT; 79 AA.
ID Q8CC23
AC Q8CC23;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Unknown EST (Fragment).
GN PTPRD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK034067; BAC28569.1; -.
DR MGD; MGI:97812; Ptpqd.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003595; PTPC motif.
DR InterPro; IPR000387; TYR_Phosphatase.
DR InterPro; IPR000242; Tyr_Pp.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PTPYHPHTASE.
DR SMART; SMO0404; PTPC_motif; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
FT NON_TER 1
FT SEQUENCE 79 AA; 8970 MW; EA7CAE6839241155 CRC64;

Query Match 3.3%; Score 14; DB 11; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGTGVFI 370
|||||
Db 9 VHCAGVGTGVFI 22

RESULT 10
Q8CC54 PRELIMINARY; PRT; 93 AA.
ID Q8CC54
AC Q8CC54;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Unknown EST (Fragment).
GN PTPRD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
```

the RIKEN Genome Exploration Research Group Phase I & II Team;  
"Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs";  
Nature 420:563-573(2002).  
EMBL; AK033873; BAC28503.1; --  
MGI; 97812; Ptpd.  
GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
InterPro; IPR003595; PTPC motif.  
InterPro; IPR000387; TYR\_PTPase.  
InterPro; IPR000242; TYR\_PP.  
Pfam; PF00102; Y\_phosphatase; 1.  
PRINTS; PR00700; PRTYPHTASE.  
SMART; SM00404; PTPC\_motif; 1.  
PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
NON TER 1  
SEQUENCE 93 AA; 10642 MW; 18CCF472432BA0CD CRC64;

Query Match 3.3%; Score 14; DB 11; Length 93;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCSAGVGRGTGVFI 370  
|||||  
23 VHCSAGVGRGTGVFI 36

SULT 11  
UMZ3

Q9UMZ3 PRELIMINARY; PRT; 134 AA.  
Q9UMZ3  
01-MAY-2000 (TrEMBLrel. 13, Created)  
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
Protein tyrosine phosphatase RQ (Fragment).  
PTP-RO.  
Homo sapiens (Human).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
Dayton M.A., Blanchard K.L.;  
"Differential expression of PTPase RNAs resulting from K562  
differentiation induced by PMA";  
Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
EMBL; AF169351; AAD50277.1; --  
HSSP; P18052; 1YFO.  
GO; GO:0016787; F:hydrolase activity; IEA.  
GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
InterPro; IPR000387; TYR\_PTPase.  
Pfam; PF00102; Y\_phosphatase; 1.  
PRINTS; PR00700; PRTYPHTASE.  
SMART; SM00194; PTPC; 1.  
PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
Hydrolase.  
NON TER 1  
NON TER 134  
SEQUENCE 134 AA; 15344 MW; 65E48021FC54368C CRC64;

Query Match 3.3%; Score 14; DB 4; Length 134;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCSAGVGRGTGVFI 370  
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99 VHCSAGVGRGTGVFI 112

RESULT 12  
Q9YIX3 PRELIMINARY; PRT; 183 AA.  
AC Q9YIX3  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE SPTR3 (Fragment)  
OS Ephydria fluviatilis.  
OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;  
OC Haploclerida; Spongillidae; Ephydatia.  
OX NCBI\_TaxID=31330;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92246376; PubMed=10229569;  
RA Ono K., Suga H., Iwabe N., Kuma K., Miyata T.;  
"Multiple protein tyrosine phosphatases in sponges and explosive gene  
duplication in the early evolution of animals before the parazoan-  
eumetazoan split";  
J. Mol. Evol. 48:654-662(1999).  
DR EMBL; AB019128; BAA82561.1; --  
DR HSSP; P18052; 1YFO.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000387; TYR\_PTPase.  
DR InterPro; IPR000242; TYR\_PP.  
Pfam; PF00102; Y\_phosphatase; 1.  
PRINTS; PR00700; PRTYPHTASE.  
SMART; SM00194; PTPC; 1.  
PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
KW Hydrolase.  
FT NON TER 1  
FT NON TER 183 AA; 20507 MW; AECD7BFP661EDBEC CRC64;  
SEQUENCE 183 AA; 20507 MW; AECD7BFP661EDBEC CRC64;

Query Match 3.3%; Score 14; DB 5; Length 183;  
Best Local Similarity 100.0%; Pred. No. 3.4e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 PLLVHCSAGVGRGTG 367  
|||||  
DB 109 PLLVHCSAGVGRGTG 122

RESULT 13  
Q8C922 PRELIMINARY; PRT; 192 AA.  
AC Q8C922  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Unknown EST (Fragment).  
GN PTPRD.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
"Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs";  
Nature 420:563-573(2002).  
EMBL; AK043201; BAC31488.1; --  
DR MGI; 97812; Ptpd.  
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

R GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
R InterPro; IPR003595; PTPC motif.  
R InterPro; IPR000387; TYR\_phosphatase.  
R InterPro; IPR000242; Tyr\_PP.  
R Pfam; PF00102; Y\_phosphatase; 1.  
R PRINTS; PR00700; PRTYPHPTASE.  
R SMART; SM00194; PTPC; 1.  
R SMART; SM00404; PTPC\_motif; 1.  
R PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
R PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 1.  
R PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
R NON\_TER 1  
Q SEQUENCE 192 AA; 22551 MW; B78B194500F33B1A CRC64;  
  
Query Match 3.3%; Score 14; DB 11; Length 192;  
Best Local Similarity 100.0%; Pred.No. 3.6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Y 357 VHCSAGVGRGTGVFI 370  
|||||  
122 VHCSAGVGRGTGVFI 135  
  
RESULT 14  
52917 PRELIMINARY; PRT; 460 AA.  
Q62917;  
01-NOV-1996 (TrEMBLrel. 01, Created)  
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
LAR receptor-linked tyrosine phosphatase.  
Rattus norvegicus (Rat).  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10116;  
[1]  
SEQUENCE FROM N.A.  
STRAIN-Sprague Dawley; TISSUE-Brain;  
MEDLINE=94075340; PubMed=8253779;  
Longo F.M., Martignetti J.A., Le Beau J.M., Zhang J.S., Barnes J.P.,  
Brosius J.,  
"Leukocyte common antigen-related receptor-linked tyrosine  
phosphatase. Regulation of mRNA expression."  
J. Biol. Chem. 268:26503-26511(1993).  
EMBL; U00477; AAC04306.1; -.  
PIR; A56493; A56493.  
HSP; P18052; IYFO.  
GO; GO:0016787; P:hydrolase activity; IEA.  
GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
GO; GO:0004872; P:receptor activity; IEA.  
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
InterPro; IPR00387; TYR\_phosphatase.  
Pfam; PF00102; Y\_phosphatase; 2.  
PRINTS; PR00700; PRTYPHPTASE.  
SMART; SM00194; PTPC; 2.  
PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 2.  
PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
Hydrolase; Receptor.  
SEQUENCE 460 AA; 52989 MW; B78CB2504F1260FA CRC64;  
  
Query Match 3.3%; Score 14; DB 11; Length 460;  
Best Local Similarity 100.0%; Pred.No. 8.1e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
357 VHCSAGVGRGTGVFI 370  
|||||  
390 VHCSAGVGRGTGVFI 403

RESULT 15  
IBAS

ID Q9IBAS PRELIMINARY; PRT; 468 AA.  
AC Q9IBAS;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE RYPTPR2Aa protein (Fragment).  
GN RYPTPR2Aa.  
OS Potamotrygon motoro (South American freshwater stingray).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Squalia; Hymnosquales; Pristiorajae; Batoidae;  
OC Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.  
OX NCBI\_TaxID=86373;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20219325; PubMed=10754074;  
RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;  
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:  
RT divergence of tissue-specific isoform genes in the early evolution of  
RT vertebrates."  
RL J. Mol. Evol. 50:302-311(2000).  
DR EMBL; AB033581; BAA95188.1; -.  
DR HSSP; P18052; IYFO.  
DR GO; GO:0016787; P:hydrolase activity; IEA.  
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR00387; TYR\_phosphatase.  
DR InterPro; IPR000242; Tyr\_PP.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SM00194; PTPC; 2.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 2.  
DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
KW Hydrolase.  
FT NON\_TER 1  
SQ SEQUENCE 468 AA; 53862 MW; 0051F5E0BDD7A580 CRC64;  
  
Query Match 3.3%; Score 14; DB 13; Length 468;  
Best Local Similarity 100.0%; Pred.No. 8.2e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 357 VHCSAGVGRGTGVFI 370  
|||||  
DB 398 VHCSAGVGRGTGVFI 411  
  
Search completed: June 16, 2004, 13:32:58  
Job time : 46 secs

GenCore version 5.1.6  
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protein - protein search, using sw model

on: June 16, 2004, 13:16:15 ; Search time 59 seconds  
(without alignments)  
2040.089 Million cell updates/sec

tle: US-09-095-478A-5

fect score: 2241

quence: 1 MSSPRKVRGKTRNDDEEG.....QYQFCYEVLEVLQNLALY 426

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 1586107 seqs, 282547505 residues

tal number of hits satisfying chosen parameters: 1586107

nimum DB seq length: 0

ximum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase : A\_Geneseq\_29Jan04.\*

1: Geneseq1980s.\*

2: Geneseq1990s.\*

3: Geneseq2000s.\*

4: Geneseq2001s.\*

5: Geneseq2002s.\*

6: Geneseq2003as.\*

7: Geneseq2003bs.\*

8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2241	100.0	426	2	Aaw89249 Mouse PTP
2	2212.5	98.7	463	2	Aaw89250 Mouse PTP
3	2133	95.2	405	2	Aaw89251 Mouse PTP
4	1506	62.7	420	5	Aae14454 Human pro
5	1372.5	61.2	508	7	Ade08106 Novel pro
6	1332	59.4	412	6	Aae37996 Human kin
7	1310	58.5	398	5	ABG30845 Human tyr
8	1310	58.5	398	7	ADD89795 Human DKF
9	1310	58.5	409	7	AdE09123 Novel pro
10	1306	58.3	561	4	ABG06042 Novel hum
11	1071	47.8	261	6	Aae37994 Human kin
12	653.5	29.2	1267	4	Aag67637 Amino aci
13	653.5	29.2	1267	4	Aag67458 Amino aci
14	653	29.1	766	6	ABU70688 Human adi
15	653	29.1	2466	2	Aar71498 Human pro
16	653	29.1	2466	2	Aaw75999 Intracell
17	653	29.1	2466	3	Aay90272 Human PTP
18	653	29.1	2485	3	Aab19343 Amino aci
19	566	25.3	122	2	Aaw89252 Rat PTP10
20	506	22.6	913	2	Aaw12522 Protein t
21	506	22.6	913	2	Aay25156 Human PTP
22	506	22.6	913	5	Aag79333 PTPHL 8/
23	506	22.6	913	7	ADD22982 Human pro
24	496.5	22.2	1948	7	ADD18742 Human dis
25	496.5	22.2	1949	7	ADE57117 Human Pro

#### ALIGNMENTS

##### RESULT 1

Aaw89249

ID Aaw89249 standard; protein; 426 AA.

XX AC Aaw89249;

DT 10-MAR-1999 (first entry)

DE Mouse PTP05.

XX KW PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;

XX KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;

XX KW neurodegenerative disease; neuronal survival; Alzheimer's disease;

XX KW Parkinson's disease; Huntington's disease.

XX OS Mus sp.

XX PN WO9849317-A2.

XX PD 05-NOV-1998.

XX PF 27-APR-1998; 98WO-US008439.

XX PR 28-APR-1997; 97US-0044428P.

XX PR 20-MAY-1997; 97US-0047222P.

XX PR 11-JUN-1997; 97US-0049477P.

XX PR 11-JUN-1997; 97US-0049756P.

XX PR 18-JUN-1997; 97US-0049914P.

XX PR 23-OCT-1997; 97US-0063595P.

XX PA {SUGEN-} SUGEN INC.

XX PI Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;

XX PI Courtneidge SA, App H, Hui TH;

XX XX WPI; 1999-009434/01.

XX DR N-PSDB; AAW81744.

XX XX New nucleic acid encoding specific protein tyrosine phosphatases - useful

XX PT for identifying specific modulators for treatment and prevention of

XX PT cancer and neurodegenerative disease.

XX PS Claim 2; Page 155-157; 193pp; English.

XX CC The present invention describes isolated, enriched or purified nucleic

XX CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The

XX CC present sequence represents mouse PTP05. The above proteins, other than

XX CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify

C substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins

X Sequence 426 AA;

Query Match 100.0%; Score 2241; DB 2; Length 426;  
 Best Local Similarity 100.0%; Pred. No. 2e-204;  
 Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MSSPRKVRGKTGRDNDDEEGNSGNLNLSLPSSSQKMTPTKPIFGNKNSENVPKPSHL 60  
 b 1 MSSPRKVRGKTGRDNDDEEGNSGNLNLSLPSSSQKMTPTKPIFGNKNSENVPKPSHL 60

Y 61 SFSDKYELVYPPLESDDTETVDVSDSLRNWNSMDSETAGPSKTVSPVLSSSRLSK 120  
 b 61 SFSDKYELVYPPLESDDTETVDVSDSLRNWNSMDSETAGPSKTVSPVLSSSRLSK 120

Y 121 DTETSVSEKELTQLAQIRPLIFNSSARGAMRDCLNTLQKXELDIIREFLEQMTLPDD 180  
 b 121 DTETSVSEKELTQLAQIRPLIFNSSARGAMRDCLNTLQKXELDIIREFLEQMTLPDD 180

Y 181 FNSGNTLQNRDKNRYRDLIPYDSTVPLGKNKDYINASYIRIVNHEEYFYIATQGLPE 240  
 b 181 FNSGNTLQNRDKNRYRDLIPYDSTVPLGKNKDYINASYIRIVNHEEYFYIATQGLPE 240

Y 241 TIEDFWQWMLNKNVAMIATREIECGVIKCYSWPISLKEPLFEHFSVLETFHVTQY 300  
 b 241 TIEDFWQWMLNKNVAMIATREIECGVIKCYSWPISLKEPLFEHFSVLETFHVTQY 300

Y 301 FTVRVFOIVKSTGKSCQVHLQFTKPDHGTGPASADFFIKYVYVRKSHITGELLVHCS 360  
 b 301 FTVRVFOIVKSTGKSCQVHLQFTKPDHGTGPASADFFIKYVYVRKSHITGELLVHCS 360

Y 361 AGVGRGTGVPICVDVWFSALEKNYSFDINIVTQMKQRCGMQTKQYQFCYEIVLEVLQ 420  
 b 361 AGVGRGTGVPICVDVWFSALEKNYSFDINIVTQMKQRCGMQTKQYQFCYEIVLEVLQ 420

Y 421 NLIALY 426  
 b 421 NLIALY 426

RESULT 2  
 R089250

D AAW89250 standard; protein; 463 AA.

X C AAW89250;

X T 10-MAR-1999 (first entry)

X X Mouse PTP05 isoform #1.

X X PTP04; PTP05; PTP10; SAD; ALK-7; protein tyrosine phosphatase;

X W type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;

X W neurodegenerative disease; neuronal survival; Alzheimer's disease;

X W Parkinson's disease; Huntington's disease.

X X Mus sp.

X X W09849317-A2.

X X 05-NOV-1998.

X X

PP 27-APR-1998; 98MO-US008439.  
 XX 28-APR-1997; 97US-0044429P.  
 PR 20-MAY-1997; 97US-0047222P.  
 PR 11-JUN-1997; 97US-0049477P.  
 PR 18-JUN-1997; 97US-0049756P.  
 PR 23-OCT-1997; 97US-0049914P.  
 XX (SUGEN-) SUGEN INC.  
 XX Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D,  
 PI Courtneidge SA, App H, Hui TH;  
 PI N-PSDB; AAW81745.  
 DR WPI; 1999-009434/01.  
 XX N-PSDB; AAW81745.  
 DR New nucleic acid encoding specific protein tyrosine phosphatases - useful  
 XX for identifying specific modulators for treatment and prevention of  
 PT cancer and neurodegenerative disease.  
 PT Claim 2; Page 157-158; 193pp; English.  
 PS The present invention describes isolated, enriched or purified nucleic  
 XX acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The  
 CC present sequence represents mouse PTP05. The above proteins, other than  
 CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify  
 CC substances that modulate their activity (i.e. agonists and antagonists,  
 CC including NBP) in vivo or in vitro. These substances are used to treat or  
 CC prevent diseases associated with abnormal signal transduction pathways  
 CC that involve the proteins, particularly cancer (e.g. leukaemia and  
 CC lymphoma), while modulators of ALK-7 (which is a type I receptor  
 CC serine/threonine kinase) are used to promote neuronal survival.  
 CC particularly for treating Alzheimer's, Parkinson's or Huntington's  
 CC diseases. Nucleic acid fragments of the polynucleotides encoding the  
 CC proteins can be used as probes to identify and clone related sequences;  
 CC to detect protein-encoded RNA; to generate transgenic animals and in gene  
 CC therapy (optionally after mutation). Ab are used to determine the  
 CC proteins

XX Sequence 463 AA;

Query Match 98.7%; Score 2212.5; DB 2; Length 463;  
 Best Local Similarity 92.0%; Pred. No. 1.2e-201;  
 Matches 456; Conservative 0; Mismatches 0; Indels 37; Gaps 1;

QY 1 MSSPRKVRGKTGRDNDDEEGNSGNLNLSLPSSSQKMTPTKPIFGNKNLMKYBEHL 60  
 DB 1 MSSPRKVRGKTGRDNDDEEGNSGNLNLSLPSSSQKMTPTKPIFGNKNLMKYBEHL 60

QY 44 -----IFGNKNSENVPKPSHLSPSSQKMTPTKPIFGNKNLMKYBEHL 83  
 DB 61 VFLLIKTIWYVFKLWKGLIFGNKNSENVPKPSHLSPSSQKMTPTKPIFGNKNLMKYBEHL 120

QY 84 DYSDSLRNWNSMDSETAGPSKTVSPVLSSSRLSKDTSVSEKELTQLAQIRPLIF 143  
 DB 121 DYSDSLRNWNSMDSETAGPSKTVSPVLSSSRLSKDTSVSEKELTQLAQIRPLIF 180

QY 144 SSARGAMRDCLNTLQKXELDIIREFLEQMTLPDDFNSGNTLQNRDKNRYRDLIPYD 203  
 DB 181 SSARGAMRDCLNTLQKXELDIIREFLEQMTLPDDFNSGNTLQNRDKNRYRDLIPYD 240

QY 204 TVPLGKNKDYINASYIRIVNHEEYFYIATQGLPETIEDFWQWMLNKNVAMITRE 263  
 DB 241 TVPLGKNKDYINASYIRIVNHEEYFYIATQGLPETIEDFWQWMLNKNVAMITRE 300

QY 264 IECGVIKCYSWPISLKEPLFEHFSVLETFHVTQYFTVRVFOIVKSTGKSCQVHLQ 323  
 DB 301 IECGVIKCYSWPISLKEPLFEHFSVLETFHVTQYFTVRVFOIVKSTGKSCQVHLQ 360

QY 324 FTKWPDHGTGPASADFFIKYVYVRKSHITGELLVHCSAGVGRGTGVPICVDVWFSA 383  
 DB 361 FTKWPDHGTGPASADFFIKYVYVRKSHITGELLVHCSAGVGRGTGVPICVDVWFSA 420

384 SFDDIMNIVTQMKQKCGMIQTKQYQFCYEVLEVLQMLLALY 426  
|||||  
421 SFDDIMNIVTQMKQKCGMIQTKQYQFCYEVLEVLQMLLALY 463

RESULT 3  
W89251  
AAW89251 standard; protein; 405 AA.

AAW89251;  
10-MAR-1999 (first entry)  
Mouse PTP05 isoform #2.

PTP04; PTP05; PTP10; SAD; ALK-7; protein tyrosine phosphatase;  
type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;  
neurodegenerative disease; neuronal survival; Alzheimer's disease;  
Parkinson's disease; Huntington's disease.

Mus sp.

WO9849317-A2.

05-NOV-1998.

27-APR-1998; 98WO-US008439.

28-APR-1997; 97US-0044428P.  
20-MAY-1997; 97US-0047222P.  
11-JUN-1997; 97US-0049477P.  
11-JUN-1997; 97US-0049756P.  
18-JUN-1997; 97US-0049914P.  
23-OCT-1997; 97US-0063595P.

(SUGE-) SUGEN INC.

Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;  
Courtneidge SA, App H, Hui TH;  
WPI; 1999-009434/01.  
N-PSDB; AAW81746.

New nucleic acid encoding specific protein tyrosine phosphatases - useful  
for identifying specific modulators for treatment and prevention of  
cancer and neurodegenerative disease.

Claim 2; Page 158-160; 193pp; English.

The present invention describes isolated, enriched or purified nucleic  
acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The  
present sequence represents mouse PTP05. The above proteins, other than  
ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify  
substances that modulate their activity (i.e. agonists and antagonists,  
including NBP) in vivo or in vitro. These substances are used to treat or  
prevent diseases associated with abnormal signal transduction pathways  
that involve the proteins, particularly cancer (e.g. leukaemia and  
lymphoma), while modulators of ALK-7 (which is a type I receptor  
serine/threonine kinase) are used to promote neuronal survival,  
particularly for treating Alzheimer's, Parkinson's or Huntington's  
diseases. Nucleic acid fragments of the polynucleotides encoding the  
proteins can be used as probes to identify and clone related sequences;  
to detect protein-encoded RNA; to generate transgenic animals and in gene  
therapy (optionally after mutation). Ab are used to determine the  
proteins

Sequence 405 AA;

Query Match 95.2%; Score 2133; DB 2; Length 405;  
Best Local Similarity 100.0%; Pred. No. 3.7e-194;  
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSPRKVRGKTGRDNDEEGNSGNLNLNSLPSSSQKMTPTKPIFGNKNSENKVPSEHL 60  
|||  
Db 1 MSSPRKVRGKTGRDNDEEGNSGNLNLNSLPSSSQKMTPTKPIFGNKNSENKVPSEHL 60  
|||  
QY 61 SFSDKYELVYPEPLESDTDTVWDVSDRLNRNWSMDSETAGPSKTVSPVLSGSSRLSK 120  
|||  
Db 61 SFSDKYELVYPEPLESDTDTVWDVSDRLNRNWSMDSETAGPSKTVSPVLSGSSRLSK 120  
|||  
QY 121 DTETSVSEKELTQLAQIRPLIFNSARGAMRDCLNTLQKKEELDIREFLEQWTLRDD 180  
|||  
Db 121 DTETSVSEKELTQLAQIRPLIFNSARGAMRDCLNTLQKKEELDIREFLEQWTLRDD 180  
|||  
QY 181 FNSGNTLQNRDKNRYRDLIPYDSTRVPLGKKNKYNINASYIRIVNHEBEFYIATQGPLPE 240  
|||  
Db 181 FNSGNTLQNRDKNRYRDLIPYDSTRVPLGKKNKYNINASYIRIVNHEBEFYIATQGPLPE 240  
|||  
QY 241 TTIEDFWQVLENNCNVIMITRETECGVIKCYSWPISLKEPLEFHFVPLETFHVTQY 300  
|||  
Db 241 TTIEDFWQVLENNCNVIMITRETECGVIKCYSWPISLKEPLEFHFVPLETFHVTQY 300  
|||  
QY 301 FTVRVFOIVKXSTGKSCVQKHLQFTKWPDHGTSPASADFFIKYVYVRKSHITGELLVHCS 360  
|||  
Db 301 FTVRVFOIVKXSTGKSCVQKHLQFTKWPDHGTSPASADFFIKYVYVRKSHITGELLVHCS 360  
|||  
QY 361 AGVGTGVFICVDVVFSAIEKNYSFDIMNIVTQMKQKCGMIQTK 405  
|||  
Db 361 AGVGTGVFICVDVVFSAIEKNYSFDIMNIVTQMKQKCGMIQTK 405  
|||

RESULT 4

AAE14454

ID AAE14454 standard; protein; 420 AA.

XX AC AAE14454;

XX 26-MAR-2002 (first entry)

XX Human protein phosphatase-4.

XX Human; protein phosphatase; PP-4; immune system disorder; AIDS; allergy;  
neurological disorder; developmental disorder; Alzheimer's disease;  
cell proliferative disorder; Huntington's disease; arteriosclerosis;  
renal tubular acidosis; gonadal dysgenesis; cancer; adenocarcinoma;  
leukaemia; transgenic animal; gene therapy.

OS Homo sapiens.

XX

Key Location/Qualifiers

Region 183..411

FT Active-site /note= "Protein-tyrosine phosphatase"

FT /note= "Tyrosine specific protein phosphatase active site"

Region 351..363

FT Domain /note= "Tyr\_phosphatase"

FT /label= Transmembrane\_domain

WO200196546-A2.

XX

PD 20-DEC-2001.

XX 14-JUN-2001; 2001WO-US019442.

PR 16-JUN-2000; 2000US-0212447P.

PR 22-JUN-2000; 2000US-0213746P.

PR 29-JUN-2000; 2000US-0215210P.

PR 06-JUL-2000; 2000US-0216529P.

PR 12-JUL-2000; 2000US-0218090P.

PR 21-JUL-2000; 2000US-0220117P.

XX (INCY-) INCYTE GENOMICS INC.

PA

XX





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b 94 SPLRLCVNDYEGNDSEAD-----LNFREALPSSQENTPRSKVFNKVNSEKVKLSLRN 148
Y 61 SFSDKVELYVPEPLESDTDETVWVDSRLNRWNSMDSETAGPSKTVSPVLSSGSRLSK 120
b 149 FPHNDYEDVFEEPSGSDPSMWTAAGPFRRDRWSEDEEAAGPSQALSPLLS----- 201
Y 121 DTETSVSEKELTQAIRPLIFNNSARSAMDCLNTLQKK-EELDIIRFELEQMTLPD 179
b 202 DTRKIVSEGLDQLAIRPLIFNFEHQTAIKDLSEKTAAYDIMGQFMALEKKNLPG 261
Y 180 DFNSGNTLQNRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHHEEYFYIATQGPLP 239
b 262 EYFSGNQPSNREKKNRYRDLIPYDSTRVPLGSKDYINASYIRIVNCGSEYFYIATQGPLL 321
Y 240 ETIEDFWQVLENNQNVIAMITRETECGVICKVYWPISLKEPELEFEHFSVPLETFHTVQ 299
b 322 STIDDFWQVLENNQNVIAMITRETECGVICKVYWPISLKEPELEHPRVPLENYQLQ 381
Y 300 YFTVRVQIVKSGTSGKQCVKHLQFTKMPDHGTPTASADFFIKYVRYVRKSHITGPLLHVC 359
b 382 YFIIRFQVVEKSTGTSKSVKQLQFTKMPDHGTPTASADSFIKYIRYARKSHLTGPMVHVC 441
Y 360 SAGVGRGTGVFCVDVVFSAIEKNYSFDIMNIVTOMRKORCGMIQTKEQYQCYEIVLEVL 419
b 442 SAGIGRTGVFLCVDVVFCAIVKNCSPNIMDIVAQMREQRSGMWQTRQYHFCYDIVLEVL 501
Y 420 QMLLAL 425
b 502 RKLLTL 507

```

## RESULT 6

AE37996  
D AAEE37996 standard; protein; 412 AA.

K AE37996;

K 06-NOV-2003 (first entry)

K Human kinase and phosphatase (KPP-41) protein.

K Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis;  
K atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer;  
K psoriasis; thrombocytopenia; developmental disorder; Reiter's syndrome;  
K renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease;  
K neurological disorder; inflammatory disorder; epilepsy; glomerulonephritis;  
K autoimmune disorder; Parkinson's disease; Goodpasture's syndrome;  
K acquired immune deficiency syndrome; immunosuppressive; Crohn's disease;  
K allergic; gout; Grave's disease; Hashimoto's thyroiditis; diabetes mellitus;  
K osteoporosis; rheumatoid arthritis; Sjogren's syndrome; opthalmological;  
K gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.

K Homo sapiens.

K WO2003050084-A2.

K 19-JUN-2003.

K 06-DEC-2002; 2002WO-US039126.

K 07-DEC-2001; 2001US-0340235P.

K 19-DEC-2001; 2001US-0343007P.

K 21-DEC-2001; 2001US-0343546P.

K 04-FEB-2002; 2002US-0354389P.

K 15-FEB-2002; 2002US-0357675P.

K (INCYTE) INCYTE GENOMICS INC.

K Kable AE, Chien D, Wilson AD, Swarnakar A, Gorvad AE;

K Hafalia AJA, Emerling BM, Ramkumar J, Jin P, Griffin JA, Marquis JP;

K Baughn MR, Chawla NK, Lehr-Nason PM, Khare R, Lee S, Hawkins PR;

PI Becha SD, Lee SY, Sprague WW, Zebarjadian Y;

XX WPI; 2003-532894/50.

DR N-PSDB; AAD57368.

XX New human kinases and phosphatases and polynucleotides, useful for  
PT diagnosing, treating or preventing autoimmune or inflammatory disorders  
PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,  
PT cancer or hepatitis.

XX Claim 1; Page 243-244; 282pp; English.

PS The invention relates to an isolated polypeptide, which is a human kinase  
XX and phosphatase (KPP). KPP agonists and antagonists are useful for  
CC diagnosing, treating or preventing disorders associated with aberrant  
CC expression of KPP, particularly cell proliferative disorders (e.g.  
CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, psoriasis,  
CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary  
CC thrombocytopenia or cancer), developmental disorders (e.g. renal tubular  
CC acidosis, anaemia or mental retardation), neurological disorders (e.g.  
CC Alzheimer's disease, Parkinson's disease or epilepsy) autoimmune/  
CC inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome,  
CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's  
CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,  
CC gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome,  
CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's  
CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,  
CC bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP  
CC is useful in assessing the effects of exogenous compounds on the  
CC expression of nucleic acids and kinases and phosphatases. KPP gene is  
CC useful in gene therapy and for creating transgenic animals to model human  
CC disease. The present sequence is human KPP protein  
XX

SQ Sequence 412 AA;

Query Match 59.4%; Score 1332; DB 6; Length 412;

Best Local Similarity 63.6%; Pred. No. 8.4e-118;

Matches 259; Conservative 51; Mismatches 89; Indels 8; Gaps 2;

```

QY 1 MSSPRKVRKTKGRDNDEEGNSGNLNLNSLPSSSQKMTPTKPIFGNKNSENVKPSHHL 60
Db 1 MSSPRDFRAEPVNDYEGNDSEADLNFRETLFSSSQENTPRSKVFNKVNSEKVLRLN 60
QY 61 SFSDKVELYVPEPLESDTDETVWVDSRLNRWNSMDSETAGPSKTVSPVLSSGSRLSK 120
Db 61 FPHNDYEDVFEEPSGSDPSMWTAAGPFRRDRWSEDEEAAGPSQALSPLLS----- 113
QY 121 DTETSVSEKELTQAIRPLIFNNSARSAMDCLNTLQKK-EELDIIRFELEQMTLPD 179
Db 114 DTRKIVSEGLDQLAIRPLIFNFEHQTAIKDLSEKTAAYDIMGQFMALEKKNLPG 173
QY 180 DFNSGNTLQNRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHHEEYFYIATQGPLP 239
Db 174 EYFSGNQPSNREKKNRYRDLIPYDSTRVPLGSKDYINASYIRIVNCGSEYFYIATQGPLL 233
QY 240 ETIEDFWQVLENNQNVIAMITRETECGVICKVYWPISLKEPELEFEHFSVPLETFHTVQ 299
Db 234 STIDDFWQVLENNQNVIAMITRETECGVICKVYWPISLKEPELEHPRVPLENYQLQ 293
QY 300 YFTVRVQIVKSGTSGKQCVKHLQFTKMPDHGTPTASADFFIKYVRYVRKSHITGPLLHVC 359
Db 294 YFIIRFQVVEKSTGTSKSVKQLQFTKMPDHGTPTASADSFIKYIRYARKSHLTGPMVHVC 353
QY 360 SAGVGRGTGVFCVDVVFSAIEKNYSFDIMNIVTOMRKORCGMIQTKEQYQCYEIVLEVL 406
Db 354 SAGIGRTGVFLCVDVVFCAIVKNCSPNIMDIVAQMREQRSGMWQTRQYHFCYDIVLEVL 400

```

## RESULT 7

ABC30845

ID ABC30845 standard; protein; 398 AA.

XX

AC ABC30845;





X Homo sapiens.  
 X WO200175067-A2.  
 X 11-OCT-2001.  
 X 30-MAR-2001; 2001WO-US0008631.  
 X 31-MAR-2000; 2000US-00540217.  
 X 23-AUG-2000; 2000US-00649167.  
 X (HYSE-) HYSEQ INC.  
 X Dmanac RT, Liu C, Tang YT;  
 X WPI; 2001-639362/73.  
 X N-PSDB; AAS70229.  
 X New isolated polynucleotide and encoded polypeptides, useful in  
 T diagnostics, forensics, gene mapping, identification of mutations  
 T responsible for genetic disorders or other traits and to assess  
 T biodiversity.  
 X Claim 20; SEQ ID NO 36401; 103pp; English.  
 X The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 C sequences. (I) is useful as hybridisation probes, polymerase chain  
 C reaction (PCR) primers, oligomers, and for chromosome and gene mapping.  
 C and in recombinant production of (II). The polynucleotides are also used  
 C in diagnostics as expressed sequence tags for identifying expressed  
 C genes. (I) is useful in gene therapy techniques to restore normal  
 C activity of (II) or to treat disease states involving (II). (II) is  
 C useful for generating antibodies against it, detecting or quantitating a  
 C polypeptide in tissue, as molecular weight markers and as a food  
 C supplement. (II) and its binding partners are useful in medical imaging  
 C of sites expressing (II). (I) and (II) are useful for treating disorders  
 C involving aberrant protein expression or biological activity. The  
 C polypeptide and polynucleotide sequences have applications in  
 C diagnostics, forensics, gene mapping, identification of mutations  
 C responsible for genetic disorders or other traits to assess biodiversity  
 C and to produce other types of data and products dependent on DNA and  
 C amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic  
 C amino acid sequences of the invention. Note: The sequence data for this  
 C patent did not appear in the printed specification, but was obtained in  
 C electronic format directly from WIPO at  
 C ftp.wipo.int/pub/published\_pct\_sequences

Query Match 58.3%; Score 1306; DB 4; Length 561;  
 Best Local Similarity 65.8%; Pred. No. 4.1e-115;  
 Matches 252; Conservative 48; Mismatches 75; Indels 8; Gaps 2;

44 IFGNKNSNVKPSHLSFSDKELYVPLPSDDTETWVDSRLNRNWSMDSETAG 103  
 185 VFENKVNSEKVKLSLRPNPHNDYEDVFEPSSGSDPSNWTARGPFRDRWSSEDEAAG 244  
 104 PSKTVPVLSGSSRLSKDTSTSVSEKLTQLAQIRLEPIENSARSAMDCLNTLQKK-EE 162  
 245 PSQALSPFLS-----DTRKIVSEGLQLQAIPLIFNPFHQETAKDKLLEKTA 297  
 163 LDIRFLEQLQWTLPPDDNSGNLTQNRNRYRDLIPYDSTRVPLGNKKNYINASYIRI 222  
 298 YDIQMSEFMALKNLPGFVSGNPSNREKNRYRDLIPYDSTRVPLGSKSDYINASYIRI 357  
 223 VNEBEVEFYATOGPIETEDPMQWLNKCNVAMITRECCGVKCYSWPLSLKEP 282  
 358 VNGCEEYFYATGPIPLSTIDDPQWLVNENKVMAMITREMEGLIKCIYFWPLSLK 417  
 283 LEPEHFSVFLETHTVYQYFTVRVFIQVKKSTGKSCVKELQFTKWPDHGTSPASADFFIKY 342  
 418 LELKHFVPLENYQILQYFIIRMFQVVEKSTGTSVSKQLQFTKWPDHGTSPASADFFIKY 477

QY 343 VRVRKSHITGPLLHCSAGVGTGVPICVDVVFAIEKQVSDIMNIVTOMKQRCGM 402  
 Db 478 IRVARKSLHTGPMVHCSAGIGTGTGVLCDVVVFAIVDCSFNIMDIVAQREQRSGW 537  
 QY 403 QTKEQYQPCYEIVLEVLQNLAL 425  
 Db 538 QTKEQYHFCYDIVLEVLRLKLLT 560

## RESULT 11

AAE37994  
 ID AAE37994 standard; protein; 261 AA.  
 XX AC AAE37994;  
 DT 06-NOV-2003 (first entry)  
 XX Human kinase and phosphatase (KPP-39) protein.

XX Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis;  
 KW atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer;  
 KW psoriasis; thrombocytopenia; developmental disorder; Reiter's syndrome;  
 KW renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease;  
 KW neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis;  
 KW autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome;  
 KW acquired immune deficiency syndrome; immunosuppressive; Crohn's disease;  
 KW neutropenic; dermatitis; multiple sclerosis; diabetes mellitus;  
 KW allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome;  
 KW osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological;  
 KW gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.

XX Homo sapiens.

XX WO2003050084-A2.

XX 19-JUN-2003.

XX 06-DEC-2002; 2002WO-US039126.

XX 07-DEC-2001; 2001US-0340235P.

XX 19-DEC-2001; 2001US-0343007P.

XX 21-DEC-2001; 2001US-0343546P.

XX 04-FEB-2002; 2002US-0354388P.

XX 15-FEB-2002; 2002US-0357675P.

XX (INCY-) INCYTE GENOMICS INC.

XX Kable AB, Chien D, Wilson AD, Swarnakar A, Swarnakar A, Gorvad AB;  
 PI Hafalia AJA, Emerling BM, Rankumar J, Jin P, Griffin JA, Marquis JP;  
 PI Baughn MR, Chawla NK, Lehr-Mason PM, Khare R, Lee S, Hawkins PR;  
 PI Becha SD, Lee SY, Sprague WW, Zebarjadian Y;

XX WPI; 2003-532894/50.

XX N-PSDB; AAD57366.

XX New human kinases and phosphatases and polynucleotides, useful for  
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders  
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,  
 PT cancer or hepatitis.

XX Claim 1; Page 242; 282pp; English.

XX The invention relates to an isolated polypeptide, which is a human kinase  
 CC and phosphatase (KPP). KPP agonists and antagonists are useful for  
 CC diagnosing, treating or preventing disorders associated with aberrant  
 CC expression of KPP, particularly cell proliferative disorders (e.g.  
 CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal  
 CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary  
 CC thrombocytopenia or cancer), developmental disorders (e.g. renal tubular  
 CC acidosis, anaemia or mental retardation), neurological disorders (e.g.  
 CC Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/  
 CC inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome,



X 28-JUL-2000; 2000WO-JF005060.  
 X 29-JUL-1999; 99JP-00248036.  
 X 18-OCT-1999; 99US-0159590P.  
 X 11-JAN-2000; 2000JP-00118776.  
 X 17-FEB-2000; 2000US-0183322P.  
 X 02-MAY-2000; 2000JP-00183767.  
 X (HELI-) HELIX RES INST.  
 X Ota T, Isoai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 I Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Punahashi S;  
 I Senoo C, Nezu J;  
 X WPI; 2001-564736/63.  
 X New genes encoding protein kinase and protein phosphatase, useful for  
 T identifying modulators which can be used to treat human or animal  
 T disorders associated with the expression or function of these enzymes.  
 X  
 X Example 4; Page 305-315; 336pp; Japanese.  
 X The specification describes human protein kinase/protein phosphatases.  
 C The polypeptides are expected to participate in signal transduction in  
 C cells, the kinase phosphatases are connected with intracellular  
 C signalling pathways. Antisense oligonucleotides and compounds identified  
 C by screening (agonists or antagonists) can be used to treat human or  
 C animal disorders associated with the expression or function of the  
 C protein. In addition, the polypeptides may be used as target molecules  
 C for drug development. The present sequence represents a polypeptide, used  
 C in the course of the invention  
 X  
 X Sequence 1267 AA;  
 X  
 X Query Match 29.2%; Score 653.5; DB 4; Length 1267;  
 X Best Local Similarity 34.7%; Pred. No. 2.3e-52;  
 X Matches 149; Conservative 73; Mismatches 152; Indels 55; Gaps 9;  
 Y 6 KVRGKTGRDNDEEGNSGNLRLNSLP---SSSQQTPTKPIFGNKNMSENVPKSHLSF 62  
 b 872 KNGKLSERTEDTDCDG-----SPLPEYFTEATKNGCEYCEBKVKSESL----- 918  
 Y 63 SDKYELVPEPLESDTDETVMDVSDRLNRNWSMDSETAGSKTVSPVLSGSRSLSKDT 122  
 b 919 -----LQKQEKKTDDDEITWG-NELPIERTNHEDSD-----KD- 952  
 Y 123 ETSVSEKLTQLAQIRPLIFNSSARSAMDCLNTLQ-----KKEELDIIRFLELEQMT 176  
 b 953 HSPLTNDELAVLPVVKVLPSPGKYTGANKLSVIRVLVARSGIPSKELNQLKPLDQCL 1012  
 Y 177 LPDDFNSGNTLONRDNRYEDILPYDSTVPLGKNKDYINASYIRIVNHERYFYIATQG 236  
 b 1013 I-----GQTKENRRNRKYNILPDYATKVPDGGGVINASFIKIPGKBEFYVIAQGG 1066  
 Y 237 PLPETIEDFQWLVNENCNVAMITREIECGVICKVSYWPISL-KEPLEFPHFSVFLETF 295  
 b 1067 PLPTTWDGFWQMIWEQSVIAMIQTQVEGEKIKQRYWENILGNTWVSNRLALVRM 1126  
 Y 296 HVTQYETVRVFQIVKSKTSQCVHQLQTPKPDHGTPTASADFFIKYVRYVRKSHITGPL 355  
 b 1127 QQUKGFVVRAMTLEDITQREVRIHSHLNTAWPDHDTSPQDLDLTFISVNRHTRSGPI 1186  
 Y 356 LVHCSAGVGTGVFICVDVVVFAIGRNVSFDMNIVTQVRKQRCMIOTKQYOCFYCIV 415  
 b 1187 ITHCSAGIGSGTLICIDVVLGLISQDLDFDLSLVRCKLRQKRWVTEQYIFCYQVI 1246  
 Y 416 LVVLQNLIA 424  
 b 1247 LVVLTLQQA 1255

RESULT 14

ABU70688  
 ID ASU70688 standard; protein; 766 AA.  
 AC ASU70688;  
 XX 10-JUN-2003 (first entry)  
 DT  
 XX Human adipocyte Selected Interacting domain, SID, #319.  
 DE  
 XX Human; prey; adipocyte; SID; selected interacting domain; anorectic;  
 XX antidiabetic; protein-protein interaction; diabetes;  
 XX yeast 2-hybrid assay; metabolic disorder; obesity.  
 OS Homo sapiens.  
 XX WO200286122-A2.  
 XX 31-OCT-2002.  
 XX 14-MAR-2002; 2002WO-EP003768.  
 XX 14-MAR-2001; 2001US-0275734P.  
 XX (HYBR-) HYBRIGENICS.  
 PA Legrain P, Daviet L;  
 XX WPI; 2003-103412/09.  
 XX N-PSDB; ACA57232.  
 PT New complex between two interacting proteins in adipocyte cells, useful  
 PT for identifying selected interacting domains that modulate protein  
 PT interactions, or for preventing or treating metabolic disorders such as  
 PT obesity or diabetes.  
 XX Claim 6; Page 208-209; 382pp; English.  
 CC The invention relates to a complex between two interacting proteins in  
 CC adipocyte cells, given in the specification. The proteins are identified  
 CC by selecting a bait protein from a known adipocyte marker and then  
 CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by  
 CC members of an adipocyte cDNA library. The proteins are designated as a  
 CC (RTM) (selected interacting domains) proteins. Also included are a  
 CC polynucleotide encoding a polypeptide in the adipocyte cells, a  
 CC recombinant host cell expressing at least one of the interacting  
 CC polypeptides of the complex, selecting a modulating compound in adipocyte  
 CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid  
 CC sequences given in the specification (including its fragment or variant),  
 CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences  
 CC given in the specification (including its fragment or variant), a vector  
 CC comprising the SID (RTM) polynucleotide, a recombinant host cell  
 CC comprising the vector, a protein chip comprising the polypeptides and a  
 CC record comprising all or part of the data, listed in the specification.  
 CC The complex, polypeptides, polynucleotides and compounds are useful for  
 CC preventing or treating metabolic disorders such as obesity or diabetes.  
 CC The polynucleotides are useful as probes or primers. The complex is  
 CC particularly useful for identifying selected interacting domains (SID  
 CC (RTM)) for screening drugs that modulate the protein interaction, thus  
 CC exhibiting the therapeutic effect. The present sequence represents a SID  
 CC (prey) protein of the invention  
 XX  
 XQ Sequence 766 AA;  
 Query Match 29.1%; Score 653; DB 6; Length 766;  
 Best Local Similarity 34.7%; Pred. No. 1.2e-52;  
 Matches 149; Conservative 73; Mismatches 152; Indels 56; Gaps 9;  
 Y 6 KVRGKTGRDNDEEGNSGNLRLNSLP---SSSQQTPTKPIFGNKNMSENVPKSHLSF 62  
 b 370 KNGKLSERTEDTDCDG-----SPLPEYFTEATKNGCEYCEBKVKSESL----- 416  
 Y 63 SDKYELVPEPLESDTDETVMDVSDRLNRNWSMDSETAGSKTVSPVLSGSRSLSKDT 122

```

> 417 -----IQKPEKKTDDDELITWG-NDELPIERTNHEDSD-----KD- 450
> 123 ETSVSEKELTQIAQIRPLIFNSSARSAMRDCINTLIQ-----KKELDIIRREPLEEQM 175
> 451 HSFLTNDELAVLPVVKVLPVVKVLTGANKLSVIRVLRGLDQGPSKELENQELKPLDQC 510
> 176 TLPDDFNSGNTLQNRDKNRYRDIILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQ 235
> 511 LI-----GQTKENARKKRYKNILPYDATRVPLGDEGGYINASFIPVKGEEFYIACQ 564
> 236 GLPETIEDFWQVLENNCNVIAITRIEIEGCVIKCYSWPISL-KPPEFEPHPSVLET 294
> 565 GLPPTTVGDFWQMIWEQKSTVIAMWTQVEGEKIKCQRYWNIIGKTTWNSRNLRLALVR 624
> 295 FHVTOYFTRVRFQIVKSTGKSCQVKHLOFTKPDHGTGPASADFFIKYRVYRKSHITGP 354
> 625 MOQLKGFVVRAMTLEDIQTRVRRHISHLNTFANPDHDTFSPQDLDLLTFISYMRHHSRGP 684
> 355 LLVHCSAGVGRGVICVDVWVPSAIBKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCYEI 414
> 685 IITHCSAGIGRSGLTICIDVVLGLISQDLDFDISDLVRCMLQRHGMVQTEDQYIFCYQV 744
> 415 VLEVLQNLIA 424
> 745 ILYVLTRLOA 754

> RESULT 15
> AAR71498 standard; protein; 2466 AA.
> AAR71498;
> 25-MAR-2003 (revised)
> 05-OCT-1995 (first entry)
> Human protein tyrosine phosphatase PTPLi.
> Protein tyrosine phosphatase; PTPLi.
> Homo sapiens.
> Key
> Region 470..505
> /label= Leucine zipper motif
> Region 570..685
> /note= "homology to the band 4.1 superfamily"
> WO9506735-A2.
> 09-MAR-1995.
> 01-SEP-1994; 94WO-US009943.
> 01-SEP-1993; 93US-00115573.
> {LUDW-} LUDWIG INST CANCER RES.
> Gopez LJ, Szasz J, Claesson-Welsh L, Heldin C;
> WPI: 1995-115450/15.
> N-PSDB; AAQ85924.
> New protein tyrosine phosphatase(s), PTPLi and GLM-2 - used to develop
> prods. for use in detection, diagnosis, screening assays or therapy.
> Claim 9; Page 56-68; 92pp; English.

```

A cDNA library was prep'd. from human glioma cell line U-343 MGA 31L or Ag1518 human foreskin fibroblasts. Degenerate primers based on conserved regions of PTPs were prep'd. Sense oligos were AAQ85926 and AAQ85927, and the antisense oligo was AAQ85928. Three clones defined novel PTP sequences. Two of these were named PTPLi and GLM-2. The U-343 MGA 31L

CC cDNA library was screened with labeled probes corresp. to PTPLi. The  
 CC AG1518 human fibroblast cDNA library was also screened. The complete ORF  
 CC of PTPLi was derived from six overlapping cDNA clones and is given in  
 CC AAQ85924. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 2466 AA;

Query Match 29.1%; Score 653; DB 2; Length 2466;

Best Local Similarity 34.7%; Pred. No. 7.3e-52;  
 Matches 149; Conservative 73; Mismatches 152; Indels 56; Gaps 9;

QY 6 KYRGVGRDNDEEGNSGNLNLNSLP---SSSQKMTPTKPIFGKNKNSENVKSHLSF 62

Db 2070 KNGKLSERTEDTDCG-----SPLPEYFTEATKMGCECYCEKVKSESL----- 2116

QY 63 SDKYELVTPPELPELSDTETVMDVSDRSLEENWNSMDSETAGFSKTVSPVLSGSSRLSKDT 122

Db 2117 -----IQKPEKKTDDDELITWG-NDELPIERTNHEDSD-----KD- 2150

QY 123 ETSVSEKELTQIAQIRPLIFNSSARSAMRDCINTLIQ-----KKELDIIRREPLEEQM 175

Db 2151 HSFLTNDELAVLPVVKVLPVVKVLTGANKLSVIRVLRGLDQGPSKELENQELKPLDQC 2210

QY 176 TLPDDFNSGNTLQNRDKNRYRDIILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQ 235

Db 2211 LI-----GQTKENARKKRYKNILPYDATRVPLGDEGGYINASFIPVKGEEFYIACQ 2264

QY 236 GLPETIEDFWQVLENNCNVIAITRIEIEGCVIKCYSWPISL-KPPEFEPHPSVLET 294

Db 2265 GLPPTTVGDFWQMIWEQKSTVIAMWTQVEGEKIKCQRYWNIIGKTTWNSRNLRLALVR 2324

QY 295 FHVTOYFTRVRFQIVKSTGKSCQVKHLOFTKPDHGTGPASADFFIKYRVYRKSHITGP 354

Db 2325 MOQLKGFVVRAMTLEDIQTRVRRHISHLNTFANPDHDTFSPQDLDLLTFISYMRHHSRGP 2384

QY 355 LLVHCSAGVGRGVICVDVWVPSAIBKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCYEI 414

Db 2385 IITHCSAGIGRSGLTICIDVVLGLISQDLDFDISDLVRCMLQRHGMVQTEDQYIFCYQV 2444

QY 415 VLEVLQNLIA 424

Db 2445 ILYVLTRLOA 2454

Search completed: June 16, 2004, 13:22:50  
 Job time : 61 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

protein - protein search, using sw model

on: June 16, 2004, 13:21:40 ; Search time 23 Seconds  
(without alignments)  
956.203 Million cell updates/sec

itle: US-09-095-478A-5

fect score: 2241

quence: 1 MSSPRKVRGKTRDNDEEG.....QYQFCYIVLEVLQNLALY 436

oring table: BLOSUM62

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sarched: 389414 seqs, 51625971 residues

tal number of hits satisfying chosen parameters: 389414

imum DB seq length: 0

aximum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- Issued Patents AA:\*  
1: /cgm2\_6/ptodata/2/iaa/5A.COMB.pep:\*  
2: /cgm2\_6/ptodata/2/iaa/5B.COMB.pep:\*  
3: /cgm2\_6/ptodata/2/iaa/6A.COMB.pep:\*  
4: /cgm2\_6/ptodata/2/iaa/6B.COMB.pep:\*  
5: /cgm2\_6/ptodata/2/iaa/PCTUS.COMB.pep:\*  
6: /cgm2\_6/ptodata/2/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	653	29.1	2465	2	US-08-596-291-3
2	653	29.1	2465	3	US-09-100-804-3
3	653	29.1	2466	3	US-09-080-855-12
4	653	29.1	2466	4	US-09-566-076-12
5	653	29.1	2466	5	PCT-US94-09943-2
6	653	29.1	2485	3	US-09-290-640-46
7	653	29.1	2485	4	US-09-665-615B-46
8	506	22.6	913	4	US-09-848-294-2
9	494	22.0	244	4	US-09-848-294-7
10	490.5	21.9	1911	1	US-08-348-006B-5
11	490.5	21.9	1911	1	US-08-800-825A-5
12	490.5	21.9	1911	3	US-09-158-657-5
13	490.5	21.9	1911	5	PCT-US94-10166-5
14	489	21.8	231	2	US-08-446-345-37
15	487	21.7	242	2	US-08-685-992-21
16	487	21.7	242	2	US-09-144-925-21
17	487	21.7	1337	3	US-08-854-595-2
18	487	21.7	1337	4	US-09-447-533-2
19	487	21.7	1337	5	PCT-US95-05312-2
20	480.5	21.4	278	1	US-08-201-697-16
21	476.5	21.3	1501	2	US-08-447-464-3
22	476.5	21.3	1501	2	US-08-716-679-3
23	475	21.2	1174	2	US-08-446-345-36
24	469	20.9	1439	2	US-08-449-644-2
25	469	20.9	1439	2	US-08-087-244A-2
26	469	20.9	1452	2	US-08-449-644-8
27	469	20.9	1452	2	US-08-087-244A-8

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Sequence 3, Appli  
Sequence 3, Appli  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 2, Appli  
Sequence 38, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 26, Appli  
Sequence 26, Appli  
Sequence 4, Appli

## ALIGNMENTS

### RESULT 1

US-08-596-291-3  
; Sequence 3, Application US/08596291  
; Patent No. 5821075  
; GENERAL INFORMATION:  
; APPLICANT: GONEZ, LEONEL JORGE  
; APPLICANT: SARAS, JAN  
; APPLICANT: CLAESON-WELSH, LENA  
; APPLICANT: HELDIN, CARL-HENRIK  
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL  
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN  
; TITLE OF INVENTION: TYROSINE PHOSPHATASES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: WOLF, GREENFIELD & SACKS, P.C.  
; STREET: 600 ATLANTIC AVENUE  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/596,291  
FILING DATE: 09-AUG-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/115,573  
FILING DATE: 01-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: GATES, EDWARD R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: L0461/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/720-3500  
TELEFAX: 617/720-2441  
TELEX: 92-1742 EZEKIEL  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2465 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-596-291-3

Query Match 29.1%; Score 653; DB 2; Length 2465;  
Best Local Similarity 34.7%; Pred. No. 1.2e-53;



Matches 149; Conservative 73; Mismatches 152; Indels 56; Gaps 9;

6 KVRGKTGRNDEEGNSGNLNLNSLP---SSQKMTPTKPIFGKKNKNSENVKPSHLSF 62

2069 KMGKLSERTEDTDCG-----SPLPEYFTEATKNGCCEYCEKVKSES- 2115

63 SDKYELVYPEPLSDTDETVWVSDRSLENRWNSMDSETAGPSKTVSPVLSSGSRSLKDT 122

2116 -----IQKPEKKTDDDEITWG-NDELPIERTNHEDSD-----KD- 2149

123 ETSVSEKELTQIAQIRPLIPNSSARGAMRDCLNTLQ-----KKEELDIIRFLELEOM 175

2150 HSFLTNDELAVLPVKVLPSPGKVTGANLKSIVIRVLGLDQGPSKELENLQELAPLQDC 2209

176 TLPDDFNSGNTLQNRDQNRDILPYDSTRVPLGKKNKYNASIRIVNHHBEYFYIATQ 235

2210 LI-----GQTKENRRKNRYKNILPYDATRVPLGDEGGYINASFIKIPVGKSEFVVIACQ 2263

236 GPLPETIEDFWQVLENNCNVIAITREIECGVVKCYSWPISL-KEPLEFPHFSVFLST 294

2264 GPLPTTVDGDFWQVLENNCNVIAITREIECGVVKCYSWPISL-KEPLEFPHFSVFLST 294

295 FHTVQYTVRVFOIVKVKSTGKSCVQKHLQFTKWPDHGTTPASADFFPKYVYVRKSHITGP 354

2324 MQQLKGFVVRAMTLEDIQTREVRHSHLNFATWPDHDTSPQDLDLITPSYMRHHRSGP 2383

355 LLVHCSAGVGTGVFCVDVWVFSALBKNSYSDIMNVTQMRKORCMQTKQYQFCYEI 414

2384 IITHCSAGIGRSCTLICIDVWLGSLISQDLDFDISDLVRCMLQRHGMVQTEQYIFCYQV 2443

415 VLRLQNLQA 424

2444 ILVLTQLQA 2453

## RESULT 2

S-09-100-804-3

Sequence 3, Application US/09100804

Patent No. 6066472

GENERAL INFORMATION:

APPLICANT: GONZ, LEONEL JORGE

APPLICANT: SARAS, JAN

APPLICANT: CLAESON-WELSH, LENA

APPLICANT: HELDIN, CARL-HENRIK

TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL

TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASES

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.

STREET: 600 ATLANTIC AVENUE

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/100,804

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/596,291

FILING DATE: 09-AUG-1996

APPLICATION NUMBER: US 08/115,573

FILING DATE: 01-SEP-1993

PRIOR APPLICATION DATA: PCT/US94/09943

APPLICATION NUMBER: PCT/US94/09943

FILING DATE: 01-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: GATES, EDWARD R.

REGISTRATION NUMBER: 31,616

REFERENCE/DOCKET NUMBER: LO461/7003

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2465 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-100-804-3

Query Match 29.1%; Score 653; DB 3; Length 2465;

Best Local Similarity 34.7%; Pred. NO. 1.2e-53;

Matches 149; Conservative 73; Mismatches 152; Indels 56; Gaps 9;

6 KVRGKTGRNDEEGNSGNLNLNSLP---SSQKMTPTKPIFGKKNKNSENVKPSHLSF 62

2069 KMGKLSERTEDTDCG-----SPLPEYFTEATKNGCCEYCEKVKSES- 2115

63 SDKYELVYPEPLSDTDETVWVSDRSLENRWNSMDSETAGPSKTVSPVLSSGSRSLKDT 122

2116 -----IQKPEKKTDDDEITWG-NDELPIERTNHEDSD-----KD- 2149

123 ETSVSEKELTQIAQIRPLIPNSSARGAMRDCLNTLQ-----KKEELDIIRFLELEOM 175

2150 HSFLTNDELAVLPVKVLPSPGKVTGANLKSIVIRVLGLDQGPSKELENLQELAPLQDC 2209

176 TLPDDFNSGNTLQNRDQNRDILPYDSTRVPLGKKNKYNASIRIVNHHBEYFYIATQ 235

2210 LI-----GQTKENRRKNRYKNILPYDATRVPLGDEGGYINASFIKIPVGKSEFVVIACQ 2263

236 GPLPETIEDFWQVLENNCNVIAITREIECGVVKCYSWPISL-KEPLEFPHFSVFLST 294

2264 GPLPTTVDGDFWQVLENNCNVIAITREIECGVVKCYSWPISL-KEPLEFPHFSVFLST 294

295 FHTVQYTVRVFOIVKVKSTGKSCVQKHLQFTKWPDHGTTPASADFFPKYVYVRKSHITGP 354

2324 MQQLKGFVVRAMTLEDIQTREVRHSHLNFATWPDHDTSPQDLDLITPSYMRHHRSGP 2383

355 LLVHCSAGVGTGVFCVDVWVFSALBKNSYSDIMNVTQMRKORCMQTKQYQFCYEI 414

2384 IITHCSAGIGRSCTLICIDVWLGSLISQDLDFDISDLVRCMLQRHGMVQTEQYIFCYQV 2443

415 VLRLQNLQA 424

2444 ILVLTQLQA 2453

RESULT 3

US-09-080-855-12

Sequence 12, Application US/09080855A

Patent No. 6083721

GENERAL INFORMATION:

APPLICANT: SARAS, JAN

APPLICANT: FRANZ, PETRA

APPLICANT: ASPENSTRIM, PONTUS

APPLICANT: HELLMAN, ULF

APPLICANT: GONZ, LEONEL JORGE

APPLICANT: HELDIN, CARL-HENRIK

TITLE OF INVENTION: PARQ, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1

FILE REFERENCE: LO461/7030

CURRENT APPLICATION NUMBER: US/09/080,855A

FILING DATE: 1998-05-18

EARLIER APPLICATION NUMBER: 08/805,583

EARLIER FILING DATE: 1997-02-25

NUMBER OF SEQ ID NOS: 39

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 12

LENGTH: 2466

TYPE: PRT  
ORGANISM: Homo sapiens  
I-09-080-855-12

Query Match 29.1%; Score 653; DB 3; Length 2466;  
Best Local Similarity 34.7%; Pred. No. 1.2e-53;  
Matches 149; Conservative 73; Mismatches 152; Indels 56; Gaps 9;  
6 KVRGKTGRDNDEEGNSGNLRLNSLP---SSSQMTFTKPIFGNKXNSNVKPSHLSF 62  
2070 KMGKLSERTEDTDCD-----SPLPEYFTEATKMGCEYCEKVKSSL----- 2116

53 SDKVELVYPEPLESDTDTVDVSDRLNRWNSMDSETAGPSKTVSPVLSGSSRLSKDT 122  
2117 -----IQPKQEKKTDDDDITWG-NDELPFIERTNHEDSD-----KD- 2150

123 ETSVSEKELTOLAQIRPLIFNSSARSAMRDCNLTLQ-----KKEBLDIIRBFELEQM 175  
2151 HSFLTNDELAVLPVVKVLPSCGYTGANKLSVIRVLRGLDQGIPSKELNLQELKPLDQC 2210

176 TLDDFNSGNTLQNRDKNRYDILPYDSTRVPLGKNKYINASVIRVWHEEYFYIATQ 235  
2211 LI-----GOTKENRRKNRYKNILPYDATRVPLDDEGGYNASFIKIPVGKEEFVYIACQ 2264

236 GLPETIEDFQWMLNKNVMIATREIECGVIKCYSPISL-KEPLBFEHFSVELET 294  
2265 GLPFTTVGDFQMWIWEQKSTVIAMTQVEGEKIKCQRYWENILGKTTMVSNNRLRLALVR 2324

295 FHVTOYFTRVRFQIVKKSQCKVHLQFTKWDHGTDPASADFFIKYRVYRKSHITGP 354  
2325 MQQLKGFVVRAMTLEDIQTRVHRHISHLNFTAWPDHDTSPQDDLLTFISYMRHHRSGP 2384

355 LLVHCSAGWGTVGFIQVDVVFSAIEKNYSFDIMNIVTQMKQKRCGMIOTKBOYQFCYEI 414  
2385 IITHCSAGIGRSGLICIDVVLGISQDLDFDISLVRQMLQRHGMVQIEDQIIFYQV 2444

415 VLEVLQNL 424  
2445 ILVVLTRLOA 2454

SUJT 4  
I-09-566-076-12  
Sequence 12, Application US/09566076  
Patent No. 6475775  
GENERAL INFORMATION:  
APPLICANT: Saras, Jan  
APPLICANT: Franzen, Petra  
APPLICANT: Aspenstrm, Pontus  
APPLICANT: Hellman, Ulf  
APPLICANT: Gopez, Leonel Jorge  
APPLICANT: Heldin, Carl-Henrik  
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1  
FILE REFERENCE: L0461/7030  
CURRENT APPLICATION NUMBER: US/09/566,076  
CURRENT FILING DATE:  
EARLIER APPLICATION NUMBER: 09/080,855  
EARLIER FILING DATE: 1998-05-18  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 12  
LENGTH: 2466  
TYPE: PRT  
ORGANISM: Homo sapiens  
I-09-566-076-12

Query Match 29.1%; Score 653; DB 4; Length 2466;  
Best Local Similarity 34.7%; Pred. No. 1.2e-53;  
Matches 149; Conservative 73; Mismatches 152; Indels 56; Gaps 9;  
6 KVRGKTGRDNDEEGNSGNLRLNSLP---SSSQMTFTKPIFGNKXNSNVKPSHLSF 62  
2070 KMGKLSERTEDTDCD-----SPLPEYFTEATKMGCEYCEKVKSSL----- 2116

QY 63 SDKVELVYPEPLESDTDTVDVSDRLNRWNSMDSETAGPSKTVSPVLSGSSRLSKDT 122  
DB 2117 -----IQPKQEKKTDDDDITWG-NDELPFIERTNHEDSD-----KD- 2150  
QY 123 ETSVSEKELTOLAQIRPLIFNSSARSAMRDCNLTLQ-----KKEBLDIIRBFELEQM 175  
DB 2151 HSFLTNDELAVLPVVKVLPSCGYTGANKLSVIRVLRGLDQGIPSKELNLQELKPLDQC 2210  
QY 176 TLDDFNSGNTLQNRDKNRYDILPYDSTRVPLGKNKYINASVIRVWHEEYFYIATQ 235  
DB 2211 LI-----GOTKENRRKNRYKNILPYDATRVPLDDEGGYNASFIKIPVGKEEFVYIACQ 2264  
QY 236 GLPETIEDFQWMLNKNVMIATREIECGVIKCYSPISL-KEPLBFEHFSVELET 294  
DB 2265 GLPFTTVGDFQMWIWEQKSTVIAMTQVEGEKIKCQRYWENILGKTTMVSNNRLRLALVR 2324  
QY 295 FHVTOYFTRVRFQIVKKSQCKVHLQFTKWDHGTDPASADFFIKYRVYRKSHITGP 354  
DB 2325 MQQLKGFVVRAMTLEDIQTRVHRHISHLNFTAWPDHDTSPQDDLLTFISYMRHHRSGP 2384  
QY 355 LLVHCSAGWGTVGFIQVDVVFSAIEKNYSFDIMNIVTQMKQKRCGMIOTKBOYQFCYEI 414  
DB 2385 IITHCSAGIGRSGLICIDVVLGISQDLDFDISLVRQMLQRHGMVQIEDQIIFYQV 2444  
QY 415 VLEVLQNL 424  
DB 2445 ILVVLTRLOA 2454

RESULT 5  
PCT-US94-09943-2  
Sequence 2, Application PC/TUS9409943  
GENERAL INFORMATION:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL  
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09943  
FILING DATE: 01-SEP-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/115,573  
FILING DATE: 01-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: TWOMEY, MICHAEL J.  
REGISTRATION NUMBER: P-38,349  
REFERENCE/DOCKET NUMBER: L0461/7000WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/720-3500  
TELEFAX: 617/720-2441  
TELEX: 92-1742 EZEKIEL  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2466 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
CT-US94-09943-2

Query Match 29.1%; Score 653; DB 5; Length 2466;  
Best Local Similarity 34.7%; Pred. No. 1.2e-53;  
Matches 149; Conservative 73; Mismatches 152; Indels 56; Gaps 9;  
y 6 KVRGKGRDNDEEGNSGNLNLSLP-----SSSQKMTPTKPIFGNKNSENKVPKSHLSF 62  
b 2070 KMGKLSERTEDTDCG-----SPLPYFTATKNGCEEYCBKVKSESL-----2116  
y 63 SKYELVYPEPLESDTDETVWDVSDRSLENRNWNSMDSETAGPSKTVSPVLSGSSRLSKDT 122  
b 2117 -----IQKQEKKTDDDEITWG-NDELPPIERTNHEDSD-----KD-2150  
y 123 ETSVSEKELTQLAQIRPLIFNSSARSAMDCLNTLQ-----KKEELDIIRFLELEQM 175  
b 2151 HSFLTNDLAVLPVWVLPSPGKYTGANKLSVIRVLRGLLDQGIKPSKELENLQELKPLDQC 2210  
y 176 TLDDFNSGNTLQNRDKRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQ 235  
b 2211 LI-----GQTKENRKNRYKNILPYDAITRVPLGDEGGVYNASFIKIPVGKEEFYIACQ 2264  
y 236 GLPETIEDFWQVLENNCNVIAMITREIECGVIKCYSWPISL-KPELEPEHFSVFLET 294  
b 2265 GLPTTVGDFWQVMEQKSTVIAMTQVEGEKIKQRYWPNILGKTTMVSNNRLRLALVR 2324  
y 295 FHTQYFTVRVFOIVKSKGKQCVKHLQFTWPDHGTTPASADFFIKYRVVRKSHITGP 354  
b 2325 MOOLKGFVVRAMTLEDIQTREVRHISHLNFTAWPDHDTFSPQDDLLTFTISYMRHHRSGP 2384  
y 355 LVHCSAGVGRGVTCVVDVPSAIEKNYSFDMNIVTQMRKQRCMIQTKEQYQFCYEI 414  
b 2385 IITHCSAGIGRSGTLICIDVVLGLISQDLDFDISLVCMLQRHGMVQTSQYIFCYQV 2444  
y 415 VLEVLQNLQA 424  
b 2445 ILYVLTRELQA 2454

RESULT 6  
S-09-290-640-46  
Sequence 46, Application US/09290640  
Patent No. 6204055  
GENERAL INFORMATION:  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Marcussen, Eric G.  
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
FILE REFERENCE: ISPH-0351  
CURRENT APPLICATION NUMBER: US/09/290,640  
CURRENT FILING DATE: 1999-04-12  
NUMBER OF SEQ ID NOS: 85  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 46  
LENGTH: 2485  
TYPE: PRT  
ORGANISM: Homo sapiens  
IS-09-290-640-46

Query Match 29.1%; Score 653; DB 3; Length 2485;  
Best Local Similarity 34.7%; Pred. No. 1.2e-53;  
Matches 149; Conservative 73; Mismatches 152; Indels 56; Gaps 9;  
y 6 KVRGKGRDNDEEGNSGNLNLSLP-----SSSQKMTPTKPIFGNKNSENKVPKSHLSF 62  
b 2089 KMGKLSERTEDTDCG-----SPLPYFTATKNGCEEYCBKVKSESL-----2135  
y 63 SKYELVYPEPLESDTDETVWDVSDRSLENRNWNSMDSETAGPSKTVSPVLSGSSRLSKDT 122  
b 2136 -----IQKQEKKTDDDEITWG-NDELPPIERTNHEDSD-----KD-2169  
y 123 ETSVSEKELTQLAQIRPLIFNSSARSAMDCLNTLQ-----KKEELDIIRFLELEQM 175

Db 2170 HSFLTNDLAVLPVWVLPSPGKYTGANKLSVIRVLRGLLDQGIKPSKELENLQELKPLDQC 2229  
Qy 176 TLDDFNSGNTLQNRDKRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQ 235  
Db 2230 LI-----GQTKENRKNRYKNILPYDAITRVPLGDEGGVYNASFIKIPVGKEEFYIACQ 2283  
Qy 236 GLPETIEDFWQVLENNCNVIAMITREIECGVIKCYSWPISL-KPELEPEHFSVFLET 294  
Db 2284 GLPTTVGDFWQVMEQKSTVIAMTQVEGEKIKQRYWPNILGKTTMVSNNRLRLALVR 2343  
Qy 295 FHTQYFTVRVFOIVKSKGKQCVKHLQFTWPDHGTTPASADFFIKYRVVRKSHITGP 354  
Db 2344 MOOLKGFVVRAMTLEDIQTREVRHISHLNFTAWPDHDTFSPQDDLLTFTISYMRHHRSGP 2403  
Qy 355 LVHCSAGVGRGVTCVVDVPSAIEKNYSFDMNIVTQMRKQRCMIQTKEQYQFCYEI 414  
Db 2404 IITHCSAGIGRSGTLICIDVVLGLISQDLDFDISLVCMLQRHGMVQTSQYIFCYQV 2463  
Qy 415 VLEVLQNLQA 424  
Db 2464 ILYVLTRELQA 2473

Query Match 29.1%; Score 653; DB 4; Length 2485;  
Best Local Similarity 34.7%; Pred. No. 1.2e-53;  
Matches 149; Conservative 73; Mismatches 152; Indels 56; Gaps 9;  
y 6 KVRGKGRDNDEEGNSGNLNLSLP-----SSSQKMTPTKPIFGNKNSENKVPKSHLSF 62  
Db 2089 KMGKLSERTEDTDCG-----SPLPYFTATKNGCEEYCBKVKSESL-----2135  
Qy 63 SKYELVYPEPLESDTDETVWDVSDRSLENRNWNSMDSETAGPSKTVSPVLSGSSRLSKDT 122  
Db 2136 -----IQKQEKKTDDDEITWG-NDELPPIERTNHEDSD-----KD-2169  
Qy 123 ETSVSEKELTQLAQIRPLIFNSSARSAMDCLNTLQ-----KKEELDIIRFLELEQM 175  
Db 2170 HSFLTNDLAVLPVWVLPSPGKYTGANKLSVIRVLRGLLDQGIKPSKELENLQELKPLDQC 2229  
Qy 176 TLDDFNSGNTLQNRDKRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQ 235  
Db 2230 LI-----GQTKENRKNRYKNILPYDAITRVPLGDEGGVYNASFIKIPVGKEEFYIACQ 2283  
Qy 236 GLPETIEDFWQVLENNCNVIAMITREIECGVIKCYSWPISL-KPELEPEHFSVFLET 294  
Db 2284 GLPTTVGDFWQVMEQKSTVIAMTQVEGEKIKQRYWPNILGKTTMVSNNRLRLALVR 2343  
Qy 295 FHTQYFTVRVFOIVKSKGKQCVKHLQFTWPDHGTTPASADFFIKYRVVRKSHITGP 354  
Db 2344 MOOLKGFVVRAMTLEDIQTREVRHISHLNFTAWPDHDTFSPQDDLLTFTISYMRHHRSGP 2403

355 LLVHCSAGVGRGTGICVDVWVSAIEKNYSFDIMNIVTQMKQRCGMQTKQYQFCYBI 414  
2404 ITHCSAGIGRSGETLICIDVGLISQDLDFDLSVRCXQLQRBHGVQTEQYIFCYQV 2463  
415 VLEVQNLLA 424  
2464 ILYVLTRLOA 2473

3500-848-294-2  
Sequence 2, Application US/09848294  
Patent No. 6479640  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas K.  
TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el  
TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal  
TITLE OF INVENTION: Adhesions and Uses Therefor  
FILE REFERENCE: CSHL90-04FZA  
CURRENT APPLICATION NUMBER: US/09/848,294  
CURRENT FILING DATE: 2001-05-03  
PRIOR APPLICATION NUMBER: 09/235,251  
PRIOR FILING DATE: 1999-01-22  
PRIOR APPLICATION NUMBER: 08/759,536  
PRIOR FILING DATE: 1996-12-04  
PRIOR APPLICATION NUMBER: 08/107,420  
PRIOR FILING DATE: 1993-08-16  
PRIOR APPLICATION NUMBER: 07/663,579  
PRIOR FILING DATE: 1991-03-01  
PRIOR APPLICATION NUMBER: 07/494,036  
PRIOR FILING DATE: 1990-03-14  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 913  
TYPE: PRT  
ORGANISM: Homosapiens  
3-09-848-294-2

Query Match 22.6%; Score 506; DB 4; Length 913;  
Best Local Similarity 32.3%; Pred. No. 4.6e-40;  
Matches 140; Conservative 63; Mismatches 163; Indels 68; Gaps 15;

13 RNDREBNGNLENLNSLPSSSQWTKPIEGKXNSKVS--HHLSFSKVELVY 70  
512 RTTPDEGKFG--FNKGGV---DQXN---PLVSRINPSPATCIPKNEGQIVLIN 563  
71 PEPLESDTDYVWVSDRSLENRNWNSMDSETAGPKTYSVPLSGSRSLKSDTETSSEKE 130  
564 GRDISEHTDQV-----VMTKASRSHSRELALVTRRAVRSFADPKSEDE 610  
131 LTQLAIRPLIFNSSARSAMRDL--NTLQKKEELDIIEZLELEOM-----T 176  
611 LNQL--FPRAIFPMCPEGG--DTLEGMAQLKGLSEGTVLIOFEQLYRKPKGLAITFAK 666  
177 LPDDFNSGNTLQNRDKNRYRDLIPDSTRVPLGKNKDYINASYI-----RIVNHEEY 229  
667 LP-----QNLDKNRYKVDLPDTRVLLQGNEDYINASYNMEIPAAVLNK---- 713  
230 FYIATQGLPETIEDFWQVLENNCNVMIATREICGVKCYSWPISLKEPLEFEH-- 287  
714 -YIATQGLPHTCAQFWQVWQDKLSLIVMLTTLTERGRTKCHQWY---DPPDVMMHGG 769  
288 FSVFLETFHTVQYFTRVFIQVVKKGTSQCCKVHLQFTKPDHGTTPASADFFIKYVYVKS 347  
770 FHQOSECTIAYVSREMLVTNTQTGEHTVTHLQYVAMPDHGIPDDSSDFLEFVYVR 829  
348 KSHI--TGPLLVHCSAGVGRGTGICVDVWVSAIEKNYSFDIMNIVTQMKQRCGMQTK 406  
830 SLRVDSEPLVHCSAGIGRTGLVMTMETAMCLTERNLPIYPLDIVRKMDQRAMVQTS 889  
407 QYQFCYEVILEVLQ 420

890 QYKFVCEAILRVYE 903

RESULT 9  
US-09-848-294-7  
; Sequence 7, Application US/09848294  
; Patent No. 6479640  
; GENERAL INFORMATION:  
; APPLICANT: Tonks, Nicholas K.  
; TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el  
; TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal  
; TITLE OF INVENTION: Adhesions and Uses Therefor  
; FILE REFERENCE: CSHL90-04FZA  
; CURRENT APPLICATION NUMBER: US/09/848,294  
; CURRENT FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: 09/235,251  
; PRIOR FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 08/759,536  
; PRIOR FILING DATE: 1996-12-04  
; PRIOR APPLICATION NUMBER: 08/107,420  
; PRIOR FILING DATE: 1993-08-16  
; PRIOR APPLICATION NUMBER: 07/663,579  
; PRIOR FILING DATE: 1991-03-01  
; PRIOR APPLICATION NUMBER: 07/494,036  
; PRIOR FILING DATE: 1990-03-14  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Homosapiens  
US-09-848-294-7

Query Match 22.0%; Score 494; DB 4; Length 244;  
Best Local Similarity 41.7%; Pred. No. 8.1e-40;  
Matches 101; Conservative 38; Mismatches 85; Indels 18; Gaps 5;

189 NRDKNRYRDLIPDSTRVPLGKNKDYINASYI-----RIVNHEEYFIATQGLPET 241  
1 NUDKNRYKVDLPDTRVLLQGNEDYINASYNMEIPAAVLNK-----YIATQGLPHT 55  
242 IEDFWQVLENNCNVMIATREICGVKCYSWPISLKEPLEFEH--PSVFLETFHTVQ 299  
56 CAQFWQVWQDKLSLIVMLTTLTERGRTKCHQWY---DPPDVMMHGGFHIQCOSEDC 112  
300 YFTVRVFIQVVKKGTSQCCKVHLQFTKPDHGTTPASADFFIKYVYVKS 358  
113 AYVSREMLVTNTQTGEHTVTHLQYVAMPDHGIPDDSSDFLEFVYVRS 172  
359 CSAGVGRGTGICVDVWVSAIEKNYSFDIMNIVTQMKQRCGMQTKQYQFCYEVILEV 418  
173 CSAGIGRTGLVMTMETAMCLTERNLPIYPLDIVRKMDQRAMVQTS 232  
419 LQ 420  
233 YE 234

RESULT 10  
US-08-348-006B-5  
; Sequence 5, Application US/08348006B  
; Patent No. 5658756  
; GENERAL INFORMATION:  
; APPLICANT: RODAN, GIDEON A.  
; APPLICANT: SCHMIDT, AZRIEL  
; APPLICANT: RUTLEDGE, SU JANE  
; TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN  
; TITLE OF INVENTION: TYROSINE PHOSPHATASE  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: J. MARK HAND  
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000  
; CITY: RAYWAY



SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/158,657

## FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/800,825

FILING DATE: 14-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: HAND, J. MARK

REGISTRATION NUMBER: 36,545

REFERENCE/DOCKET NUMBER: 18992DA

TELEPHONE: 732-594-3905

TELEFAX: 732-594-4720

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1911 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-10166-5

Query Match 21.9%; Score 490.5; DB 3; Length 1911;  
Best Local Similarity 40.2%; Pred. No. 4.9e-38;  
Matches 107; Conservative 47; Mismatches 91; Indels 21; Gaps 7;

170 LLEQWTLRDD-----FNSGNTLQNRDKRYRDLIPYDSTRVPLG-----KMKDYINAS 218  
1643 MELEFKRLANSKAHSTRISANLPCCKFKNLVNIIMPYESTVCLQPIRGVSGSDYINAS 1702  
219 YIRIVNHBEEYFIATQGLPETIEDFWQVLENNCNVMIATREIECGVTKCYSPIS 278  
1703 FID--GYRQKAYIATQGLPETIEDFWQVLENNCNVMIATREIECGVTKCYSPIS 1758  
279 LKPELEFHFVSF--LETHVTQYFTVRVQIVKSGSCVKKLQFTKWDHGTGPASAD 337  
1759 AERSARYQVYFVVDPAEYNNPQYI--LRBFKVTARDGQSRVTRQFQFTDPEQGVPSGE 1817  
338 FPKYRVYRKSH-----ITGPLLVHCSAGVGRGTGVICVDVVSFAIEKNYSFDMNIVTQ 393  
1818 GFIDFPGVHKTKQEGQGGPISVHCSAGVGRGTGVITLSVLRMRYEGVVDIFQVTKM 1877  
394 MKRQCGMIQTKEQYQFCYEIVLEVL 419  
1878 LRTQRPAMVQTEDEYQFCYQAAYL 1903

## RESULT 13

US-09-095-478a-5

Sequence 5, Application PC/TUS9410166

GENERAL INFORMATION:

APPLICANT: RODAN, GIDEON A

APPLICANT: SCHMIDT, AZRIEL

APPLICANT: RUTLEDGE, SU JANE

TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASE

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESS: JOHN W. WALLEN III

STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.

CITY: RAYWAY

STATE: NJ

COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/10166

FILING DATE: 09-SEPT-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/122,032

FILING DATE: 14-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: WALLEN, JOHN W III

REGISTRATION NUMBER: 35403

REFERENCE/DOCKET NUMBER: 18992

TELEPHONE: 908-594-3905

TELEFAX: 908-594-4720

TELEX: 138825

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1911 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-10166-5

Query Match 21.9%; Score 490.5; DB 5; Length 1911;  
Best Local Similarity 40.2%; Pred. No. 4.9e-38;  
Matches 107; Conservative 47; Mismatches 91; Indels 21; Gaps 7;

170 LLEQWTLRDD-----FNSGNTLQNRDKRYRDLIPYDSTRVPLG-----KMKDYINAS 218  
1643 MELEFKRLANSKAHSTRISANLPCCKFKNLVNIIMPYESTVCLQPIRGVSGSDYINAS 1702  
219 YIRIVNHBEEYFIATQGLPETIEDFWQVLENNCNVMIATREIECGVTKCYSPIS 278  
1703 FID--GYRQKAYIATQGLPETIEDFWQVLENNCNVMIATREIECGVTKCYSPIS 1758  
279 LKPELEFHFVSF--LETHVTQYFTVRVQIVKSGSCVKKLQFTKWDHGTGPASAD 337  
1759 AERSARYQVYFVVDPAEYNNPQYI--LRBFKVTARDGQSRVTRQFQFTDPEQGVPSGE 1817  
338 FPKYRVYRKSH-----ITGPLLVHCSAGVGRGTGVICVDVVSFAIEKNYSFDMNIVTQ 393  
1818 GFIDFPGVHKTKQEGQGGPISVHCSAGVGRGTGVITLSVLRMRYEGVVDIFQVTKM 1877  
394 MKRQCGMIQTKEQYQFCYEIVLEVL 419  
1878 LRTQRPAMVQTEDEYQFCYQAAYL 1903

## RESULT 14

US-08-446-345-37

Sequence 37, Application US/08446345

Patent No. 5831009

GENERAL INFORMATION:

APPLICANT: Ullrich, Axel

APPLICANT: Moller, Niels P.H.

APPLICANT: Moller, Niels P.H.

TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE

TITLE OF INVENTION: PHOSPHATASES PTP-D1

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: N.Y.

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,345

FILING DATE: 22-MAY-1995



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

1 protein - protein search, using sw model

run on: June 16, 2004, 13:24:26 / Search time 48 seconds  
(without alignments)  
2500.319 Million cell updates/sec

File: US-09-095-478A-5  
Project score: 2241  
Sequence: 1 MSSPRKVRGKTGRDNDEEG.....QYQFCYEVLEVLQNLALY 426

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Aligned: 1158786 seqs, 281726120 residues  
Total number of hits satisfying chosen parameters: 1158786

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Set-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:  
1: /cgm2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgm2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgm2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgm2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgm2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgm2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgm2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgm2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgm2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgm2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgm2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgm2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgm2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgm2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgm2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgm2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgm2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgm2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2241	100.0	426	10	US-09-095-478-1
2	2212.5	98.7	463	10	US-09-095-478-2
3	2133	95.2	412	10	US-09-095-478-3
4	1997	89.1	379	10	US-09-095-478-8
5	1862	83.1	354	10	US-09-095-478-6
6	1406	62.7	420	16	US-10-311-764-4
7	668	29.8	122	10	US-09-095-478-4
8	653.5	29.2	1267	12	US-10-060-065-35
9	653.5	29.2	1267	14	US-10-093-585-56
10	653	29.1	2466	14	US-10-177-980-12
11	653	29.1	2485	9	US-09-802-669-46
12	653	29.1	2485	12	US-10-619-220-46
13	653	29.1	2485	16	US-10-408-765A-1349
14	644.5	28.8	381	10	US-09-095-478-7
15	640	28.6	358	10	US-09-095-478-9

16 581.5 25.9 263 12 US-10-087-684-93 Sequence 93, Appl  
17 581.5 25.9 263 12 US-10-218-779-93 Sequence 93, Appl  
18 566 25.3 122 10 US-09-095-478-5 Sequence 5, Appl  
19 538 24.0 235 12 US-10-087-684-94 Sequence 94, Appl  
20 538 24.0 235 12 US-10-218-779-94 Sequence 94, Appl  
21 538 24.0 235 12 US-10-072-012-819 Sequence 819, Appl  
22 506 22.6 913 9 US-09-848-294-2 Sequence 2, Appl  
23 506 22.6 913 14 US-10-293-231-2 Sequence 2, Appl  
24 506 22.6 913 14 US-10-366-547-38 Sequence 38, Appl  
25 496.5 22.2 1948 9 US-10-808-602-55 Sequence 55, Appl  
26 496.5 22.2 1948 10 US-09-800-198-45 Sequence 45, Appl  
27 495 22.1 703 15 US-10-366-547-40 Sequence 40, Appl  
28 494 22.0 244 9 US-09-848-294-7 Sequence 7, Appl  
29 494 22.0 244 14 US-10-293-231-7 Sequence 7, Appl  
30 490.5 21.9 1502 9 US-09-808-602-54 Sequence 54, Appl  
31 490.5 21.9 1502 10 US-09-800-198-44 Sequence 44, Appl  
32 487 21.7 291 9 US-09-788-626-22 Sequence 22, Appl  
33 487 21.7 1337 14 US-10-390-501-2 Sequence 2, Appl  
34 487 21.7 1337 15 US-10-366-547-42 Sequence 42, Appl  
35 487 21.7 1337 15 US-10-366-547-44 Sequence 44, Appl  
36 485 21.6 1495 15 US-10-258-666-12 Sequence 12, Appl  
37 482.5 21.5 264 14 US-10-245-539-6 Sequence 6, Appl  
38 481.5 21.5 344 16 US-10-408-765A-1670 Sequence 1670, Appl  
39 477 21.3 1463 14 US-10-176-847-22 Sequence 22, Appl  
40 477 21.3 1463 14 US-10-205-823-343 Sequence 343, Appl  
41 477 21.3 1997 10 US-09-909-567B-54 Sequence 54, Appl  
42 477 21.3 1997 16 US-10-834-027-2 Sequence 4, Appl  
43 477 21.3 1997 16 US-10-408-765A-2135 Sequence 2135, Appl  
44 476 21.2 1216 15 US-10-366-547-49 Sequence 49, Appl  
45 475 21.2 1238 15 US-10-366-547-47 Sequence 47, Appl

## ALIGNMENTS

## RESULT 1

US-09-095-478-1  
Sequence 1, Application US/09095478  
Publication No. US20030095970A1  
GENERAL INFORMATION:  
APPLICANT: Florman, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600



TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 426 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 (S-09-095-478-1)

Query Match 100.0%; Score 2241; DB 10; Length 426;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-194;  
 Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MSSPRKVRGKTGRDNDDEEGNSGNLNRSLPSSSQKMTPTKPIFGNKNNSENKVPKSHL 60  
 b 1 MSSPRKVRGKTGRDNDDEEGNSGNLNRSLPSSSQKMTPTKPIFGNKNNSENKVPKSHL 60  
 Y 61 SPSDKYELVYPEPLSDTDTVDVSDRLRNWNSMDSETAGPSKTVSPVLSSRLSK 120  
 b 61 SPSDKYELVYPEPLSDTDTVDVSDRLRNWNSMDSETAGPSKTVSPVLSSRLSK 120  
 Y 121 DTSTSVSEKELTQLAQIRPLIFNSSARSAMRDCNLTQKKEBLDIIRFLELEQMTLPDD 180  
 b 121 DTSTSVSEKELTQLAQIRPLIFNSSARSAMRDCNLTQKKEBLDIIRFLELEQMTLPDD 180  
 Y 181 FNSGNTLQNRDKNRYDILPYDSTRPLGKNKDYINASYIRVNHSEEFYIATQGPLPE 240  
 b 181 FNSGNTLQNRDKNRYDILPYDSTRPLGKNKDYINASYIRVNHSEEFYIATQGPLPE 240  
 Y 241 TISDFQWVLENNCNVIAITREIEGVIKCYSYWPISEKLEPEHFSVLETHVYQY 300  
 b 241 TISDFQWVLENNCNVIAITREIEGVIKCYSYWPISEKLEPEHFSVLETHVYQY 300  
 Y 301 FTVRVQIVKSTGKQCQVHQLQFTKWPDHGTPASADFFIKYRVYRKSHITGPILVHCS 360  
 b 301 FTVRVQIVKSTGKQCQVHQLQFTKWPDHGTPASADFFIKYRVYRKSHITGPILVHCS 360  
 Y 361 AGVGTGVFICVDVWFSATIEKNYSFDIMNIVTQMRKQRCMIQTKEQYFCYEVILEVLQ 420  
 b 361 AGVGTGVFICVDVWFSATIEKNYSFDIMNIVTQMRKQRCMIQTKEQYFCYEVILEVLQ 420  
 Y 421 NLLALY 426  
 b 421 NLLALY 426

## RESULT 2

S-09-095-478-2  
 Sequence 2, Application US/09095478  
 Publication No. US20030095970A1

## GENERAL INFORMATION:

APPLICANT: Plowman, Gregory  
 TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
 TITLE OF INVENTION: PHOSPHATASE SUPT905 AND  
 TITLE OF INVENTION: RELATED PRODUCTS AND  
 TITLE OF INVENTION: METHODS  
 NUMBER OF SEQUENCES: 25

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSeq for Windows 2.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/095,478  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:

ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 224/115  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 463 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 (US-09-095-478-2)

Query Match 98.7%; Score 2212.5; DB 10; Length 463;  
 Best Local Similarity 92.0%; Pred. No. 1.1e-191;  
 Matches 426; Conservative 0; Mismatches 0; Indels 37; Gaps 1;

Qy 1 MSSPRKVRGKTGRDNDDEEGNSGNLNRSLPSSSQKMTPTKPIFGNKNNSENKVPKSHL 43  
 Db 1 MSSPRKVRGKTGRDNDDEEGNSGNLNRSLPSSSQKMTPTKPIFGNKNNSENKVPKSHL 60  
 Qy 44 -----IFGNKNNSENKVPKSHLSPSDKYELVYPEPLSDTDTVM 120  
 Db 61 VFLLIKTIWVYVFKWKGKLIIFGNKNNSENKVPKSHLSPSDKYELVYPEPLSDTDTVM 143  
 Qy 84 DVSDRLRNWNSMDSETAGPSKTVSPVLSSGSRSLSKDTSTSVSEKELTQLAQIRPLIFN 180  
 Db 121 DVSDRLRNWNSMDSETAGPSKTVSPVLSSGSRSLSKDTSTSVSEKELTQLAQIRPLIFN 180  
 Qy 144 SSARSAMRDCNLTQKKEBLDIIRFLELEQMTLPDDFNSGNTLQNRDKNRYDILPYDS 203  
 Db 181 SSARSAMRDCNLTQKKEBLDIIRFLELEQMTLPDDFNSGNTLQNRDKNRYDILPYDS 240  
 Qy 204 TRVPLGKNKDYINASYIRVNHSEEFYIATQGPLPETIEDFQWVLENNCNVIAITRE 263  
 Db 241 TRVPLGKNKDYINASYIRVNHSEEFYIATQGPLPETIEDFQWVLENNCNVIAITRE 300  
 Qy 264 IECGVIKCYSYWPISEKLEPEHFSVLETHVYQYFTVRVQIVKSTGKQCQVHQLQ 323  
 Db 301 IECGVIKCYSYWPISEKLEPEHFSVLETHVYQYFTVRVQIVKSTGKQCQVHQLQ 360  
 Qy 324 FTKWPDHGTPASADFFIKYRVYRKSHITGPILVHCSAGVGTGVFICVDVWFSATIEKNY 383  
 Db 361 FTKWPDHGTPASADFFIKYRVYRKSHITGPILVHCSAGVGTGVFICVDVWFSATIEKNY 420  
 Qy 384 SFDIMNIVTQMRKQRCMIQTKEQYFCYEVILEVLQNLALY 426  
 Db 421 SFDIMNIVTQMRKQRCMIQTKEQYFCYEVILEVLQNLALY 463

## RESULT 3

US-09-095-478-3

Sequence 3, Application US/09095478  
 Publication No. US20030095970A1

## GENERAL INFORMATION:

APPLICANT: Plowman, Gregory  
 TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
 TITLE OF INVENTION: PHOSPHATASE SUPT905 AND  
 TITLE OF INVENTION: RELATED PRODUCTS AND  
 TITLE OF INVENTION: METHODS  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 224/115

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 412 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

S-09-095-478-3

Query Match 95.2%; Score 2133; DB 10; Length 412;

Best Local Similarity 100.0%; Pred. No. 1.5e-184;

Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y	1	MSSPRKVRGKTGRDDEEGNSGNLRLNSLSSSQKMTPTKPIFGNKNSENKVPSSHLL	60
b	1	MSSPRKVRGKTGRDDEEGNSGNLRLNSLSSSQKMTPTKPIFGNKNSENKVPSSHLL	60
Y	61	SFSDKYELVYPELESDDTETVMDVSDRLNRWNSMDSETAGPSKTVSPVLSSGSRLSK	120
b	61	SFSDKYELVYPELESDDTETVMDVSDRLNRWNSMDSETAGPSKTVSPVLSSGSRLSK	120
Y	121	DTSTVSEKELTOLAQIRPLIFNSARSARDCNLTQKKELDIIRFLEQMTLPDD	180
b	121	DTSTVSEKELTOLAQIRPLIFNSARSARDCNLTQKKELDIIRFLEQMTLPDD	180
Y	181	FNSGNTLQNRDKRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPE	240
b	181	FNSGNTLQNRDKRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPE	240
Y	241	TIEDPQWLNNKNCNVIAMITREIECGVIKCYSPFISLKEPFEHFSVLETFHTVQY	300
b	241	TIEDPQWLNNKNCNVIAMITREIECGVIKCYSPFISLKEPFEHFSVLETFHTVQY	300
Y	301	FTVRVFIQVKSSTGKSCQVKHLQFTKWPDPHGTTPASADFFIKYRVKRSHITGPLLHCS	360
b	301	FTVRVFIQVKSSTGKSCQVKHLQFTKWPDPHGTTPASADFFIKYRVKRSHITGPLLHCS	360
Y	361	AGVGRGVFCVDVWFSAEIKNYSFDIMNIVTQMRKQRCGMIOTK	405
b	361	AGVGRGVFCVDVWFSAEIKNYSFDIMNIVTQMRKQRCGMIOTK	405

RESULT 4

S-09-095-478-8

Sequence 8, Application US/09095478

Publication No. US20030095970A1

## GENERAL INFORMATION:

APPLICANT: Plowman, Gregory

TITLE OF INVENTION: NOVEL PROTEIN TYROSINE

TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND

TITLE OF INVENTION: RELATED PRODUCTS AND

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon &amp; Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/095,478

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 224/115

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 379 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-09-095-478-8

Query Match 89.1%; Score 1997; DB 10; Length 379;

Best Local Similarity 100.0%; Pred. No. 2.8e-172;

Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	46	GNKNSENKVPSSHLSFSDKYELVYPELESDDTETVMDVSDRLNRWNSMDSETAGPS	105
Db	1	GNKNSENKVPSSHLSFSDKYELVYPELESDDTETVMDVSDRLNRWNSMDSETAGPS	60
Qy	106	KTVSPVLSSGSRLSKDTETSVSEKELTOLAQIRPLIFNSARSARDCNLTQKKELDI	165
Db	61	KTVSPVLSSGSRLSKDTETSVSEKELTOLAQIRPLIFNSARSARDCNLTQKKELDI	120
Qy	166	IRSFLEBQMTLPDDPNSGNTLQNRDKRYRDLIPYDSTRVPLGKNKDYINASYIRIVNH	225
Db	121	IRSFLEBQMTLPDDPNSGNTLQNRDKRYRDLIPYDSTRVPLGKNKDYINASYIRIVNH	180
Qy	226	EEYFYIATQGPLPETIEDFWQVLNNKNCNVIAMITREIECGVIKCYSPFISLKEPFE	285
Db	181	EEYFYIATQGPLPETIEDFWQVLNNKNCNVIAMITREIECGVIKCYSPFISLKEPFE	240
Qy	286	EHPVSFLETFHTVQYFTVRVFIQVKSSTGKSCQVKHLQFTKWPDPHGTTPASADFFIKYRV	345
Db	241	EHPVSFLETFHTVQYFTVRVFIQVKSSTGKSCQVKHLQFTKWPDPHGTTPASADFFIKYRV	300
Qy	346	VRKSHITGPLLHCSAGVGTGVFCVDVWFSAEIKNYSFDIMNIVTQMRKQRCGMIOTK	405
Db	301	VRKSHITGPLLHCSAGVGTGVFCVDVWFSAEIKNYSFDIMNIVTQMRKQRCGMIOTK	360

406 EQYQFCYBIVLEVLQNLIA 424  
|||||  
361 EQYQFCYBIVLEVLQNLIA 379  
|||||

RESULT 5  
US-09-095-478-6  
Sequence 6, Application US/09095478  
Publication No. US20030095970A1  
GENERAL INFORMATION:  
APPLICANT: Plowman, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
PHOSPHATASE SUPTP65 AND  
RELATED PRODUCTS AND  
METHODS  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 354 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide

IS-09-095-478-6  
Query Match 83.1%; Score 1862; DB 10; Length 354;  
Best Local Similarity 100.0%; Pred. No. 4.4e-160;  
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

71 PEPLESTDETDVDSRLRNWNSMDSETAGSKTVSPVLSGSRSLKOTETSVSEKE 130  
1 PEPLESTDETDVDSRLRNWNSMDSETAGSKTVSPVLSGSRSLKOTETSVSEKE 60  
131 LTQAQIRPLIFNSSARSAMRDCLNTLQKBEIDIIREFLEQMTLPDDFNSGNTLQNR 190  
61 LTQAQIRPLIFNSSARSAMRDCLNTLQKBEIDIIREFLEQMTLPDDFNSGNTLQNR 120  
191 DKNRYDILPVDSTRVPLGNKYINASYIRIYNHBEETFYATQGPLTETIEDFWQVYL 250  
121 DKNRYDILPVDSTRVPLGNKYINASYIRIYNHBEETFYATQGPLTETIEDFWQVYL 180  
251 ENNCNVIAITRETCGVKCYWYPSLSKPELEPHFVSFLETHVTOYFTVRVFOIVK 310  
|||||

Db 181 ENNCNVIAITRETCGVKCYWYPSLSKPELEPHFVSFLETHVTOYFTVRVFOIVK 240  
Qy 311 KSTGKSOQVKHLOFTKWDHGTTPASADFEIKVYRVKSHITGPIIVHCSAGVGTGYFI 370  
|||||  
Db 241 KSTGKSOQVKHLOFTKWDHGTTPASADFEIKVYRVKSHITGPIIVHCSAGVGTGYFI 300  
|||||  
Qy 371 CVDVFSIAIEKNYSFDIMNIVTQMRKQRCMTQTEQYQFCYBIVLEVLQNLIA 424  
|||||  
Db 301 CVDVFSIAIEKNYSFDIMNIVTQMRKQRCMTQTEQYQFCYBIVLEVLQNLIA 354  
|||||

RESULT 6  
US-10-311-764-4  
Sequence 4, Application US/10311764  
Publication No. US20040023245A1  
GENERAL INFORMATION:  
APPLICANT: INCYTE GENOMICS, INC.; AU-YOUNG, Janice K.  
APPLICANT: BAUGHN, Mariah R.; DING, Li  
APPLICANT: ELLIOTT, Vicki S.; GANDHI, Ameena R.  
APPLICANT: GRIFFIN, Jennifer A.; HAPALIA, April J.A.  
APPLICANT: KEARNEY, Liam; LEE, Ernestine A.  
APPLICANT: LU, Yan; NGUYEN, Darniel B.  
APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi  
APPLICANT: STEWART, Elizabeth A.; TANG, Y. Tom  
APPLICANT: THORNTON, Michael B.; TRIBOULEY, Catherine M.  
APPLICANT: CRAWLA, Narinder K.; YANG, Junning  
APPLICANT: YAO, Monique G.; YUE, Henry  
TITLE OF INVENTION: PROTEIN PHOSPHATASES  
FILE REFERENCE: PI-0126 USN  
CURRENT APPLICATION NUMBER: US/10/311,764  
CURRENT FILING DATE: 2002-12-16  
PRIOR APPLICATION NUMBER: PCT/US01/19442  
PRIOR FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: US 60/212,447  
PRIOR FILING DATE: 2000-06-16  
PRIOR APPLICATION NUMBER: US 60/213,746  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: US 60/215,210  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: US 60/216,529  
PRIOR FILING DATE: 2000-07-06  
PRIOR APPLICATION NUMBER: US 60/218,080  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/220,117  
PRIOR FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PERL Program  
SEQ ID NO 4  
LENGTH: 420  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. US20040023245A1 7476861CD1  
US-10-311-764-4

Query Match 62.7%; Score 1406; DB 16; Length 420;  
Best Local Similarity 64.1%; Pred. No. 1.2e-118;  
Matches 273; Conservative 53; Mismatches 92; Indels 8; Gaps 2;

Qy 1 MSSPRKVRGTGDRNDEEGNSGNLNRSLPSSSQKMTPTKPIFGNKNSENVKPSHEL 60  
Db 1 MSSPRFRAEPVNDYDGNDSABDLNFRETLPSSSQENTPRSKVPKNSENVKSLRN 60  
Qy 61 SFSDPKVELVYPELESDTDTETVWDVSDRSRLRNWNSMDSETAGSKTVSPVLSGSRSLK 120  
Db 61 PPHNDVEDVEESESSEGSDFSMWTARGPFRDRWSSDEEAAGPSQALSPLLS----- 113  
121 DTETSVSEKELTQAQIRPLIFNSSARSAMRDCLNTLQK- BELDIIREFLEQMTLPD 179  
|||||  
Db 114 DTRKIVSEGELOLAQIRPLIFNFHQTAIKOCLKLEBKTAAYDIMQEFMALEKLNLP 173  
|||||

Y 180 DFNQNTLONRDKNRYDILPYDSTREVPKGNKVDYNASYIRIVNHEEYFYIATOGPLP 239  
 b 174 EFNQGNQPNREKNRYDILPYDSTREVPKGNKVDYNASYIRIVNCGEYFYIATOGPLL 233  
 Y 240 ETIEDFWQVLENNCNV:AMITREIECGVVKICYSYWPISLKEPFEFEHFSVLETFHWQ 299  
 b 234 STIDDFWQVLENNCNV:AMITREIEGGIICVYHWPISLKPLELKHFRVLENYQILQ 293  
 Y 300 YTVRVFOIVKSTGSKQCVKHLQFTKPDHGTTPASADFFIKYVVRKSHITGPLLHVC 359  
 c 294 YFIIRMFQVVKSTGTSKQVQLQFTKPDHGTTPASADSFIKYIRYARKSHLTGPMVWHC 353  
 Y 360 SAGVGRGTGVFCVDVWFSAIEKNYSFDMNIIVTKRKORCGMIQTKQYQCYBIIVLEVL 419  
 c 354 SAGIGRTGVFLVDVWFCAIVNCSFNIMDIVAQNEDORSQVGTKEQYHFCYDIVLEVL 413  
 Y 420 QNLLAL 425  
 c 414 RKLLTL 419

## RESULT 7

S-09-095-478-4

Sequence 4, Application US/09095478

Publication No. US2003095970A1

GENERAL INFORMATION:

APPLICANT: Gregory Plozman, Gregory

TITLE OF INVENTION: NOVEL PROTEIN TYROSINE

TITLE OF INVENTION: PHOSPHATASE SUPP05 AND

TITLE OF INVENTION: RELATED PRODUCTS AND

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESSES:

ADDRESS: Lyon &amp; Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/095,478

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 224/115

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 122 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

S-09-095-478-4

Query Match

Best Local Similarity 100.0%; Pred. No. 1.6e-52;

Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 DFWQVLENNCNV:AMITREIECGVVKICYSYWPISLKEPFEHFSVLETFHWQYTV 303  
 Db 1 DFWQVLENNCNV:AMITREIECGVVKICYSYWPISLKEPFEHFSVLETFHWQYTV 60  
 QY 304 RVFOIVKSTGSKQCVKHLQFTKPDHGTTPASADFFIKYVVRKSHITGPLLHVC 363  
 Db 61 RVFOIVKSTGSKQCVKHLQFTKPDHGTTPASADFFIKYVVRKSHITGPLLHVC 120  
 QY 364 GR 365  
 Db 121 GR 122

## RESULT 8

US-10-060-065-35

Sequence 35, Application US/10060065

Publication No. US20030017480A1

GENERAL INFORMATION:

APPLICANT: Toshio Ota

APPLICANT: Takao Isogai

APPLICANT: Tetsuo Nishikawa

APPLICANT: Koji Hayashi

APPLICANT: Kaoru Otsuka

APPLICANT: Jun-ichi Yamamoto

APPLICANT: Shizuko Ishii

APPLICANT: Tomoyasu Sugiyama

APPLICANT: Ai Wakamatsu

APPLICANT: Keiichi Nagai

APPLICANT: Tetsuji Otsuki

APPLICANT: Shin-ichi Funahashi

APPLICANT: Chiaki Senoo

APPLICANT: Jun-ichi Nezu

FILE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE

CURRENT APPLICATION NUMBER: US/10/060,065

CURRENT FILING DATE: 2002-01-29

PRIOR APPLICATION NUMBER: PCT/JP00/05061

PRIOR FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: US 60/159,590

PRIOR FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: US 60/183,322

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: JP 11-248036

PRIOR FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: JP 2000-118776

PRIOR FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: JP 2000-183767

PRIOR FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: JP 2000-241899

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 35

LENGTH: 1267

TYPE: PRT

ORGANISM: Homo sapiens

US-10-060-065-35

Query Match

Best Local Similarity 29.2%; Score 653.5; DB 12; Length 1267;

Matches 149; Conservative 73; Mismatches 152; Indels 55; Gaps 9;

QY 6 KYRGKTRDNDEEGNSGNLNLNSLP---SSSQWMTPTKIFGNKNSNVKPSHLSF 62

Db 872 KWNGKLSERTDTCDCG-----SPLPYFTFYKNGCCYCEKVKVASEL----- 918

QY 63 SDKYLVPPEPLESDTDVWDVDSRLRNWNSMDSETAGTSKTVSPVLSGSRLSKDT 122

Db 919 -----IQKPEKKTDDDEITWG-NDELPIERTNEDSD-----KD- 952

QY 123 ETSVSEKELTQLAQRPLRPLFNSSASASAMRDCLNTLQ-----KKEELDIIREFLEQMT 176

Db 123 ETSVSEKELTQLAQRPLRPLFNSSASASAMRDCLNTLQ-----KKEELDIIREFLEQMT 176



176 TLDDPNSGNTLQNRKRYDILPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQ 235  
2211 LI-----GQTKENRRKRYKNILPYDATRPLGDEGGYINASFIKIPVGEFFYIACQ 2264  
236 GLPETIEDFQWMLNENCNVAMITREIECGVHKYKSYWPISL-KEPLBEHFSVPLET 294  
2265 GLPPTTVGDFQWIMEQKSTVIAMTQVEGEKIKCQRYWPNILGKTTWVSNRLRLALVR 2324  
295 FHVTOYFTRVRFQIVKSKGSCQVKHLOFTKWPDHGTTPASADFFIKYRVVRKSHITGP 354  
2325 MOQLKGFVVRAMTLEDIQTRVVRHSHLNFAMPDHTPSQPDLLTFISYMRHHRSGP 2384  
355 LLVHCSAGVGRGVFCVUDVWFSAEIKNYSFDIMNIVTQMRKQRCGMIOTKEQYQFCYEI 414  
2385 IITHCSAGIRSGTGLICIDVVLGLISQDLDFDISLVRCMRLQRHGMVQTBQYIFCYQV 2444  
415 VLEVLQNLIA 424  
2445 ILVVLTRLOA 2454

3501 11  
3-09-802-669-46  
Sequence 46, Application US/09802669  
Patent No. US2002004490A1  
GENERAL INFORMATION:  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Marcussen, Eric G.  
APPLICANT: Wyatt, Jacqueline  
APPLICANT: Zhang, Hong  
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
FILE REFERENCE: ISPH-545  
CURRENT APPLICATION NUMBER: US/09/802,669  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: US 09/665,615  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 09/290,640  
PRIOR FILING DATE: 1999-04-12  
NUMBER OF SEQ ID NOS: 180  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 46  
LENGTH: 2485  
TYPE: PRT  
ORGANISM: Homo sapiens  
1-09-802-669-46

Query Match 29.1%; Score 653; DB 9; Length 2485;  
Best Local Similarity 34.7%; Pred. No. 3.1e-49;  
Matches 149; Conservative 73; Mismatches 152; Indels 56; Gaps 9;

6 KVRGKTGRDNDEEGNSGNLNRSLP---SSSQMTPTKPIFGNKNSENKPSHLSF 62  
2089 KXNGKLSBERTEDTCDG-----SPLPEYFTEATKMGCEYCEKYKSSSL----- 2135

63 SKXYELVYPEPLESDTDTVMDVSDRSLRNWNSDGETAGPSKTVSPVLGSSRLSKOT 122  
2136 -----IQKPEKKTDDDEITWG-NDELPPIERTNHESD-----KD- 2169

123 ETSVSEKELTOLAQIRPLIFNSARSAMDCLNTLO-----KKELDIIRFLEBQW 175  
2170 HSFLNDELAVLPVVKVLPFGKYTGANKLSVIRVLGLDQGIKSKLENLQELKPLDQC 2229

176 TLDDPNSGNTLQNRKRYDILPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQ 235  
2230 LI-----GQTKENRRKRYKNILPYDATRPLGDEGGYINASFIKIPVGEFFYIACQ 2283

236 GLPETIEDFQWMLNENCNVAMITREIECGVHKYKSYWPISL-KEPLBEHFSVPLET 294  
2284 GLPPTTVGDFQWIMEQKSTVIAMTQVEGEKIKCQRYWPNILGKTTWVSNRLRLALVR 2343

295 FHVTOYFTRVRFQIVKSKGSCQVKHLOFTKWPDHGTTPASADFFIKYRVVRKSHITGP 354  
2325 MOQLKGFVVRAMTLEDIQTRVVRHSHLNFAMPDHTPSQPDLLTFISYMRHHRSGP 2384

355 LLVHCSAGVGRGVFCVUDVWFSAEIKNYSFDIMNIVTQMRKQRCGMIOTKEQYQFCYEI 414  
2445 ILVVLTRLOA 2454

2344 MOQLKGFVVRAMTLEDIQTRVVRHSHLNFAMPDHTPSQPDLLTFISYMRHHRSGP 2403  
355 LLVHCSAGVGRGVFCVUDVWFSAEIKNYSFDIMNIVTQMRKQRCGMIOTKEQYQFCYEI 414  
2404 IITHCSAGIRSGTGLICIDVVLGLISQDLDFDISLVRCMRLQRHGMVQTBQYIFCYQV 2463  
415 VLEVLQNLIA 424  
2464 ILVVLTRLOA 2473

RESULT 12  
US-10-619-220-46  
Sequence 46, Application US/10619220  
Publication No. US20040033979A1  
GENERAL INFORMATION:  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Marcussen, Eric G.  
APPLICANT: Wyatt, Jacqueline  
APPLICANT: Zhang, Hong  
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
FILE REFERENCE: ISPH-545  
CURRENT APPLICATION NUMBER: US/10/619,220  
CURRENT FILING DATE: 2003-07-14  
PRIOR APPLICATION NUMBER: 09/802,669  
PRIOR FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: US 09/665,615  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 09/290,640  
PRIOR FILING DATE: 1999-04-12  
NUMBER OF SEQ ID NOS: 180  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 46  
LENGTH: 2485  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-619-220-46

Query Match 29.1%; Score 653; DB 12; Length 2485;  
Best Local Similarity 34.7%; Pred. No. 3.1e-49;  
Matches 149; Conservative 73; Mismatches 152; Indels 56; Gaps 9;

6 KVRGKTGRDNDEEGNSGNLNRSLP---SSSQMTPTKPIFGNKNSENKPSHLSF 62  
2089 KXNGKLSBERTEDTCDG-----SPLPEYFTEATKMGCEYCEKYKSSSL----- 2135

63 SKXYELVYPEPLESDTDTVMDVSDRSLRNWNSDGETAGPSKTVSPVLGSSRLSKOT 122  
2136 -----IQKPEKKTDDDEITWG-NDELPPIERTNHESD-----KD- 2169

123 ETSVSEKELTOLAQIRPLIFNSARSAMDCLNTLO-----KKELDIIRFLEBQW 175  
2170 HSFLNDELAVLPVVKVLPFGKYTGANKLSVIRVLGLDQGIKSKLENLQELKPLDQC 2229

176 TLDDPNSGNTLQNRKRYDILPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQ 235  
2230 LI-----GQTKENRRKRYKNILPYDATRPLGDEGGYINASFIKIPVGEFFYIACQ 2283

236 GLPETIEDFQWMLNENCNVAMITREIECGVHKYKSYWPISL-KEPLBEHFSVPLET 294  
2284 GLPPTTVGDFQWIMEQKSTVIAMTQVEGEKIKCQRYWPNILGKTTWVSNRLRLALVR 2343

295 FHVTOYFTRVRFQIVKSKGSCQVKHLOFTKWPDHGTTPASADFFIKYRVVRKSHITGP 354  
2344 MOQLKGFVVRAMTLEDIQTRVVRHSHLNFAMPDHTPSQPDLLTFISYMRHHRSGP 2403

355 LLVHCSAGVGRGVFCVUDVWFSAEIKNYSFDIMNIVTQMRKQRCGMIOTKEQYQFCYEI 414  
2404 IITHCSAGIRSGTGLICIDVVLGLISQDLDFDISLVRCMRLQRHGMVQTBQYIFCYQV 2463  
415 VLEVLQNLIA 424  
2464 ILVVLTRLOA 2473

## RESULT 13

IS-10-408-765A-1349

Sequence 1349, Application US/10408765A

Publication No. US20040101874A1

## GENERAL INFORMATION:

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Zhang, Bing

APPLICANT: Gibson, Bradford W.

APPLICANT: Taylor, Steven W.

APPLICANT: Glenn, Gary M.

APPLICANT: Warnock, Dale E.

TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

FILE REFERENCE: 660088.465

CURRENT APPLICATION NUMBER: US/10/408,765A

CURRENT FILING DATE: 2003-04-04

NUMBER OF SEQ ID NOS: 3077

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1349

LENGTH: 2485

TYPE: PRT

ORGANISM: Homo sapiens

IS-10-408-765A-1349

## Query Match

Best Local Similarity 29.1%; Score 653; DB 16; Length 2485;

Matches 149; Conservative 73; Mismatches 152; Indels 56; Gaps 9;

y 6 KVRSKTRGRDNDDEEGNSGNLNLNSLP---SSSQKMTPTKPIFGKMKSENKVPKSHLSF 62

b 2089 KMGKJSEETEDTDCG-----SPUPYFTEATKNGCEYCBKVKSESLSL----- 2135

y 63 SDKELYVPFLESDDTETVMDVSDRSLRNRNMSMDSETAGPSKTVSPVLGSSRLSKDT 122

b 2136 -----IQPQEKTKTDDDEITWG-NDELPITRTNHEDSD-----KD- 2169

y 123 ETSVSEKELTQIAQIRPLINSSARSAMRDCLNTLQ-----KKEELDIIREFLEBQM 175

b 2170 HSFLTNDLAVLPVVKVLPSPGKYTGANLKSIVRLRGLLDQGIPEKLENLQELPLDQC 2229

y 176 TLPDDFNSGNTLQNRDKNRYRDLIPDSTVRPLGKNKYNASIRIVNHEEYFVIATQ 235

b 2230 LI-----GQTKENRKRYKNILPYDAETVPLGDEGGYNASFIKIPVGKEEFVYIACQ 2283

y 236 GPLPETIEDFWQWVLNKNCNVIAITREIECGVIKCVSYWPISL-KEPLEFEHFSVFLET 294

b 2284 GPLPTTVGDFWQWMEQKSTVIAMTQVEBGEKIKQRYWPNILGKTTMVSNRLRLALVR 2343

y 295 FHVTQYFTVRVFOIVKXSTGKSCQVXHLQFTKWPDHGTASADFFIKYVRYVRKSHITGP 354

b 2344 MQQLKGFVRAMTLEDIQTREVRHISHLNFTAMPDHDTPSQPDDLLTPTSYWRHTRSGP 2403

y 355 LLVHCSAGVGRGTGVCIDVWVFAIEKNYSFDIMNIVTQMKRCOMIQTKSQYQFCYEI 414

b 2404 IITHCSAGIGRSGLTICIDVVLGLISQDLDFDISDLVRQMLRQHGVMQVQTEQYIPCYQV 2463

y 415 VLEVLQNLIA 424

b 2464 ILYVLTLRQA 2473

## RESULT 14

IS-09-095-478-7

Sequence 7, Application US/09095478

Publication No. US20030095970A1

## GENERAL INFORMATION:

APPLICANT: Plowman, Gregory

TITLE OF INVENTION: NOVEL PROTEIN TYROSINE

TITLE OF INVENTION: PHOSPHATASE SUPTPOS AND

TITLE OF INVENTION: RELATED PRODUCTS AND

## TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon &amp; Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/095,478

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 224/115

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 381 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-09-095-478-7

Query Match

Best Local Similarity 28.8%; Score 644.5; DB 10; Length 381;

Matches 151; Conservative 66; Mismatches 125; Indels 51; Gaps 11;

Qy 71 PEPI-----ESDTEDEWMDV-----DRSLRNRNMSMD-SETAGPSKTVSPVLGSG 115

Db 1 PDLRTNGEAPESGTD---YDGSPLPEDVPESVSGEGKVDLASLTAASQBEKPIEEDA 57

Qy 116 SRLSKD--TETS-----VSSEKELTQIAQIRPLINSSARSAMRDCLNTLQ----- 158

Db 58 TQSRNSTTETTDGEDSSKDPPELTVEELAAPVVRVPPSGKYTGTOLOQTINTLQGLLD 117

Qy 159 --KKBELDIIRFLELEBQWTLPPDDFNSGNTLQNRDKNRYRDLIPYDSTRVPLGKNKOYI 215

Db 118 QGTPSKLENLQELKPLDQCLI-----GQTKENRKRYKNILPYDTRVPLGDEGGYI 171

Qy 216 NASYRIVNHEEYFVIATQGPLPETIEDFWQWVLNKNCNVIAITREIECGVIKCVSYW 275

Db 172 NASFIRIPVGQBFVYIACQGPLPTTVGDFWQWVWQNSQNSQVIAAMTQVEBGEKIKQORYW 231

Qy 276 PISL-KEPLEFEHFSVFLETFHTVTOYFTVRVFOIVKXSTGKSCQVXHLQFTKWPDHGTGA 334

Db 232 PSILGTTTANERLRLLALRMQQLKGFIVRVMALEDIQTGEVRHISHLNFTAMPDHDTPS 291

Qy 335 SAD---PFIKYVRYVRKSHITGPELLVHCSAGVGRGTGVCIDVWVFAIEKNYSFDIMNIV 391

Db 292 QPDDLLTFTSYMRHRRS---GPVITHCSAGIGRSGLTICIDVVLGLISQDLDFDISDLV 348

Qy 392 TOMRKQRCGMIOQKEQYQFCYETIVLEVLQNLIA 424

Db 349 RCMRLQRHGMVQTEGQYVFCYQVILYVLTLRQA 381

## RESULT 15

S-09-095-478-9  
Sequence 9, Application US/09095478  
Publication No. US20030095970A1  
GENERAL INFORMATION:  
APPLICANT: Florman, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 358 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide

3--09-095-478-9

Query Match 28.6%; Score 640; DB 10; Length 358;  
Best Local Similarity 35.9%; Pred. No. 2.7e-49;  
Matches 142; Conservative 67; Mismatches 139; Indels 48; Gaps 7;  
37 KMTPTKPIFGKNSENVKPSHLSFSDKYLVPPELESDDTETVWDVSDRSLSRNEWNS 96  
3 KANGEEYCEEKVKSES-----IQPQEKKTDDDEITWG-NDELFIERTNH 48  
97 MDSETAGPSKTVSPVLGSSRLSKDTSTSVSEKELTQLAIRPLIFNSSAPSAARDCLNT 156  
49 EDS-----KD-HSFLNDELAVLPVVKVLPSPGKYTGANKLSVIRV 88  
157 LQ-----KKEELDLIRFELEQMTLPDDFNSGNTLQNRDKRYRDILPYDSTRPLG 209  
89 LKGLLDQGIKPSKELENLQELKPLDQCLI-----GQTKENRRKRYKNILPYDAIRVPLG 142  
210 KKKDYINASYIRIVNHEEYFYIATQGLPETIEDFMQVLENNCNVMIAMITRIEGCVI 269  
143 DEGGYINASFILKIPVKEEFYVIAQGLPTTVGDFWQXIWQKSTVIAMWTQVEGEKI 202  
270 KCYSTWPSL-KEPLERHFSVLETFHTVQYFTRVRFQIVKSTGSKQCVKHLQFTKWP 328  
203 KCQRYWPNILGKTTMVSNRLRLALVRMQLKGFVVRAWMTLEDIQTREVRHISHINFTAWP 262

QY 329 DHGTPASADFFIKYVRYVRKSHITGELLVHCSAGVGRGVFCVDVWFSAEKNYSFOIM 388  
Db 263 DHDTSPQDDLLTTFISYNEHHSRSGPIITHCSAGIGRSGLTICIDVVLGLISQDLDPDIS 322  
QY 389 NIVTQMRKORCGMIQTKBOYQFCYEIVLEVLQNLLA 424  
Db 323 DEVRCNELQRHGMVQTEQYIFCYQVILYVLTQLQA 358

Search completed: June 16, 2004, 13:30:18  
Job time : 50 secs



result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1310	58.5	398	2	T08716		protein-tyrosine-p
2	657	29.3	2450	2	S71625		protein-tyrosine-p
3	653	29.1	267630	2	I67630		protein-tyrosine-p
4	653	29.1	2466	2	I67629		protein-tyrosine-p
5	645	28.8	2490	1	A54971		protein-tyrosine-p
6	522.5	23.3	1187	1	JC4155		protein-tyrosine-p
7	506	22.6	913	1	A41109		protein-tyrosine-p
8	500	22.2	1189	1	T30336		protein-tyrosine-p
9	497.5	22.2	2051	2	T30938		receptor tyrosine
10	487	21.7	1337	1	I38670		protein-tyrosine-p
11	484.5	21.6	1175	2	S51005		protein-tyrosine-p
12	483	21.6	1499	2	I50212		protein-tyrosine-p
13	481.5	21.5	1912	2	A56178		protein-tyrosine-p
14	481	21.5	1176	2	I58345		protein tyrosine p
15	479	21.4	597	2	B33978		protein-tyrosine-p
16	478.5	21.4	526	1	A41105		protein-tyrosine-p
17	477.5	21.3	1262	1	B48758		protein-tyrosine-p
18	477.5	21.3	1496	1	A48758		protein-tyrosine-p
19	477	21.3	1997	1	S12050		protein-tyrosine-p
20	476.5	21.3	1501	2	I58148		protein-tyrosine-p
21	476.5	21.3	1863	2	S46217		protein-tyrosine-p
22	475	21.2	694	2	A53978		protein-tyrosine-p
23	475	21.2	1174	2	I38140		protein-tyrosine-p
24	475	21.2	1238	2	S68700		protein-tyrosine-p
25	474.5	21.2	1156	2	T23308		hypothetical prote
26	474.5	21.2	1907	2	S50893		protein-tyrosine-p
27	472	21.1	1290	2	A56493		leucocyte common
28	470	21.0	583	2	S17671		protein-tyrosine-p
29	469	20.9	1452	1	S17669		protein-tyrosine-p

```

RESULT 2
71625
rotein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 13 - mouse
;Alternate names: epidermal growth factor-binding protein; serine proteinase
;Species: Mus musculus (house mouse)
;Date: 27-Nov-1997 #sequence revision 12-Dec-1997 #text_change 21-Jun-2002
;Accession: S71625; S67987; I81209; I81209; S40290
;Chida, D.; Kume, T.; Mukouyama, Y.; Tabata, S.; Nomura, M.L.; Watanabe, T.
ESL Lett. 358, 233-239, 1995
;Title: Characterization of a protein tyrosine phosphatase (RIP) expressed at a very ea
;Reference number: S71625, MUID:9514516; PMID:7843407
;Accession: S71625
;Molecule type: mRNA
;Residues: 1-2450 <CHI>
;Cross-references: EMBL:DB3966; NID:g1232103; PIDN:BAAL12158.1; PID:g1232104
;Experimental source: strain DBA/2; cell line MEL 745A
;Wolf, B.B.; Brown, M.D.
ESL Lett. 376, 177-180, 1995
;Title: Epidermal growth factor-binding protein activates soluble and receptor-bound si
;Reference number: S67987; MUID:96105375; PMID:7498536
;Accession: S67987
;Molecule type: protein
;Residues: 1098-1102 <WOL>
;Experimental source: submaxillary glands
;Sato, T.; Irie, S.; Kitada, S.; Reed, J.C.
Glance 268, 411-415, 1995
;Title: FAP-1: a protein tyrosine phosphatase that associates with Fas.
;Reference number: I59595; MUID:95232528; PMID:7536343
;Accession: I81210
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: mRNA
;Residues: 1329-1354, 'K' 1356-1447, 'R' 1449-1454 <RES>
;Cross-references: GB:I34582; NID:9806297; PIDN:AAQ42056.1; PID:g806298
;Accession: I81209
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: mRNA
;Residues: 1338-1354, 'K' 1356-1447, 'R' 1449-1454 <RE2>
;Cross-references: GB:I34581; NID:9806295; PIDN:AAQ42055.1; PID:g806296
;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
submitted to the EMBL Data Library, June 1993
;Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
;Reference number: S40280
;Accession: S40290
;Molecule type: mRNA
;Residues: 2266-2372 <HEN>
;Cross-references: EMBL:Z23059; NID:g438155; PIDN:CAA80594.1; PID:g438156
;Genetics:
;Gene: Ptpn13
;Map position: 5
;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
;Keywords: phosphoprotein; phosphoric monoester hydrolase; transmembrane protein; tyros
;566-860/Domain: protein 4.1 membrane-binding domain homology <B41>
;1089-1165/Domain: GLGF domain homology <GLG1>
;1361-1437/Domain: GLGF domain homology <GLG2>
;1495-1574/Domain: GLGF domain homology <GLG3>
;1769-1840/Domain: GLGF domain homology <GLG4>
;1863-1937/Domain: GLGF domain homology <GLG5>
;2203-2422/Domain: protein-tyrosine-phosphatase homology <PTP1>
;2374/Active site: Cys (phosphocysteine intermediate) #status predicted
;2380/Binding site: substrate phosphate (Arg) #status predicted

Query Match 29.3%; Score 657; DB 2; Length 2450;
Best Local Similarity 32.4%; Pred. No. 7.1e-39;
Matches 167; Conservative 75; Mismatches 154; Indels 120; Gaps 13;

y 1 MSSPGR--KVRGKTKGRNDREBEGNSGNLNRSLPSSSQKMTPTKPIFGNMNSNVK--- 55
b 1952 ISAPRFTKANGLSMB-----PSQPALMPKNSF--SKYNGEGVEAV 1992

y 56 -PSHHLSFSDKYEL-----VYPLESDTDTWVDSDSLNRNSV-- 97
b 1993 CPAGEGSSSQMKESAGLTETKESNSRDDDIYDDPQAEVIOQLLDVDEAQNLRSHA 2052

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QY 98 -----DSETAGPSKTVSPVLSSRLSK--- 120
DB 2053 TRRACSPDLRTNGEAPBEGDTDYNGSPLPEDVPESVSSGCKVDLASLTAASQEKPIE 2112
QY 121 -----DTETS-----VSEKELTOLAQIRPLIFNSSARSAMDCLNTLQ- 158
DB 2113 EDATQESRNTTETTDGESSKPPPLFNEBLAALPVVRVPSPSKYKTQTQOATIRTLQG 2172
QY 159 -----KKEELDIIRFLELEBQMTLPDDFNSGNTLQNRDKRYRDILPYDSTRVPLGKXK 212
DB 2173 LLDQGIPISELENLQBLKPLDQCLI-----GQTKENRRKRYKNILPYDTRVPLGDGEG 2226
QY 213 DYINASYIRIVNHEEYFYIATQGLPETIEDFWQVLENNCNVIAITREIECGVIKY 272
DB 2227 GYNATFIRIPVGTQGFVYIACQGLPTTVGDFWQVMEQNSTVIAMTQVBEKIKCQ 2286
QY 273 SYWPISL-KEPLEFEHFSVLETFHTVQYFTRVRFQIVKKSQSCQVKHLQFQKWPDRHG 331
DB 2287 RWPSILGTTTMANERLRLALRMQOLKGFVRVMALEDIQTGEVRHISHLNFTAMPDHD 2346
QY 332 TPASAD---FFIKYVRYVRKSHITQPLLVHCSAGVGTGVFICVDVVFSAIEKNSYSDIM 388
DB 2347 TFSQPDLLTFISYMRHRRS---GPIVTHCSAGIRSGTLICIDVVLGLISQDLBFDIS 2403
QY 389 NIWTVMRKORCGMIOTKQYQFCYEVILEVLQNLLA 424
DB 2404 DLVRCMLRQKRWQTEGQVFCYQVILVLTLOA 2439

RESULT 3
I67630
rotein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 3 -
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 30-Jun-2002
C;Accession: I67630
R;Maekawa, K.; Inagawa, N.; Nagamatsu, M.; Harada, S.
FEBS Lett. 337, 200-206, 1994
A;Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane
A;Reference number: I53483; MUID:94116679; PMID:8287977
A;Accession: I67630
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2294 <RES>
A;Cross-references: GB:D21211; NID:g452193; PIDN:BA04752.1; PID:g452194
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
C;Keywords: phosphoric monoester hydrolase
P;574-868/Domain: protein 4.1 membrane-binding domain homology <B41>
P;1182-1258/Domain: GLGF domain homology <GLG2>
P;2046-2265/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 29.1%; Score 653; DB 2; Length 2294;
Best Local Similarity 34.7%; Pred. No. 1.2e-38;
Matches 149; Conservative 73; Mismatches 152; Indels 56; Gaps 9;

QY 6 KVRGKTKGRNDREBEGNSGNLNRSLP---SSSQKMTPTKPIFGNMNSNVKPSHLSF 62
DB 1898 KMGKLSERTEDTDCG-----SLPYFTATKNGCEYCEKVSSESL----- 1944
QY 63 SDKYELVYPEPLESDTDTWVDSDSLNRNSMDSTAGSKTVSPVLSSRLSKDT 122
DB 1945 -----IQKPEKKTDDDEITWG-NDELPERTNHEDS-----KD- 1978
QY 123 ETSVSEKELTOLAQIRPLIFNSSARSAMDCLNTLQ-----KKEELDIIRFLELEBQ 175
DB 1979 HSPLTINDELAVFVVKVLPSPGKYTGANLKSIVRLRLGLLDQGIPISELENLQBLKPLDQ 2038
QY 176 TLPDDFNSGNTLQNRDKRYRDILPYDSTRVPLGKXKDYINASYIRIVNHEEYFYIATQ 235
DB 2039 LI-----GQTKENRRKRYKNILPYDTRVPLGDGEGGYINASFIKIPVGEFFVYIACQ 2092
QY 236 GPLPETIEDFWQVLENNCNVIAITREIECGVIKYCTWPISL-KEPLEFEHFSVLETF 294
DB 2093 GPLPTTVGDFWQVMEQNSTVIAMTQVBEKIKRQYFWPNTILGKTIVNSNRLALVR 2152

```

SULT 4  
7629  
otoin-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 2 -  
Species: Homo sapiens (man)  
Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 30-Jun-2002  
Accession: I67629  
Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.  
BS Lett. 337, 200-206, 1994  
Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane  
Reference number: 153483; MUID:94116679; PMID:8287977  
Accession: I67629  
Status: preliminary; translated from GB/EMBL/DBJ  
Molecule type: mRNA  
Residues: 1-2466 <RES>  
Cross-references: GB:D21210; NID:G452191; PIDN:BA04751.1; PID:G452192  
Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;  
Keywords: phosphoric monoester hydrolase  
574-868/Domain: protein 4.1 membrane-binding domain homology <B41>  
1354-1430/Domain: GLGF domain homology <GLG2>  
2218-2437/Domain: protein-tyrosine-phosphatase homology <PTP>  
Query Match 29.1%; Score 653; DB 2; Length 2466;  
Best Local Similarity 34.7%; Pred. No. 1.4e-38;  
Matches 149; Conservative 73; Mismatches 152; Indels 56; Gaps 9;  
6 KVRGKTGDRNDEEGNSGNLNRSLP---SSSKMTPTKPIFGNKNSENKVPKSHLSF 62  
2070 KNGKLSERTEDTDCG-----SPLPEYFEATKNGCEYCKEYKSESL----- 2116  
63 SDKYELVYPEFLESDTDTETWVDVDRSLRNWNSMDSETAGPKTSVPLSGSSRLSKDT 122  
2117 -----IQKPEKKTDDDEITWG-NDELPERTNHEDSD-----KD- 2150  
123 ETSVSEKELTQAIQIRPLIFNSSARSAMRDCNLTQ-----KKEELDIIIRRELEQM 175  
2151 HSFLTNDELAVLPVVKVLPSPGKYTGANKLSVIRVLRGLDQGIKPSKELENLQELKPLDQC 2210  
176 TLPPDFNSGNTLQNRDKRYRDLIPYDSTRVPLGKNKYINASVIRVWHEEYFYIATQ 235  
2211 LI-----GQIKENRKNRYKNILPYATRVPLDGEYINAFIKIPVCKEFPVLIACQ 2264  
236 GPLPTIEDFQWVLENNCNVIAITREIEGVTKVSYWPISL-KEPLFEHPSVPLET 294  
2265 GPLPTTVGDFQWVLENNCNVIAITREIEGVTKVSYWPISL-KEPLFEHPSVPLET 2324  
295 FHVQYFTRVRFQIVKSTGKSCQVXHLQFTKPDHGTPTASADFFIKYVYVRKSHITGP 354  
2325 MQQLKGFVVRAMTLEDIGQTRVRIHSHLFTAFWDHDTTPSQDDLLTFISYMRHISG 2384  
355 LIVHCSAGVGTGVPICVDVVFSAIEKNYSPDINIVYTKMKQRCGMQTKQYQCYEI 414  
2385 IITHCSAGIGSGTLICIDVVLGLISQDLDFDISLVRNLRQHGVMQVQEDQYIFCYQV 2444  
415 VLEVLQNLIA 424  
2445 ILVYLTRLQA 2454

SULT 5

A54971  
N-Alternate names: Fas-associated phosphatase FAP-1; protein-tyrosine-phosphatase hPTP1E  
C:Species: Homo sapiens (man)  
C:Date: 11-Nov-1994 #sequence\_revision 08-Feb-1996 #text\_change 21-Jun-2002  
C:Accession: A54971; A55114; I59595; I53483; S46955  
Risanville, D.; Ahmad, S.; Stocco, R.; Shen, S.H.  
J. Biol. Chem. 269, 22320-22327, 1994  
A:Title: A novel protein-tyrosine phosphatase with homology to both the cytoskeletal pro  
A:Reference number: A54971; MUID:94350988; PMID:8071359  
A:Accession: A54971  
A:Molecule type: mRNA  
A:Residues: 1-2490 <BAN>  
A:Cross-references: GB:U12128  
A>Note: sequence shown follows authors' translation at positions 62-63  
R.Saras, J.; Claesson-Welsh, L.; Heldin, C.H.; Gonez, L.J.  
J. Biol. Chem. 269, 24082-24089, 1994  
A:Title: Cloning and characterization of PTP1L, a protein tyrosine phosphatase with simi  
A:Reference number: A55114; MUID:95014139; PMID:7929060  
A:Accession: A55114  
A:Molecule type: mRNA  
A:Residues: 1-61, 'GS', 64-839, 'D', 841-1055, 1075-1133, 'FH', 1136-1210, 'I', 1212-1383, 1389-15  
A:Cross-references: GB:X80289; NID:G515030; PIDN:CAA56563.1; PID:G515031  
R.Sato, T.; Irie, S.; Kitada, S.; Reed, J.C.  
Science 268, 411-415, 1995  
A:Title: FAP-1: a protein tyrosine phosphatase that associates with Fas.  
A:Reference number: I59595; MUID:95232528; PMID:7536343  
A:Accession: I59595  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1279-1888 <RES>  
A:Cross-references: GB:L34583; NID:G806291; PIDN:AAC41755.1; PID:G806292  
R.Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.  
PDBS Lett. 337, 200-206, 1994  
A:Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane  
A:Reference number: I53483; MUID:94116679; PMID:8287977  
A:Accession: I53483  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-61, 'GS', 64-839, 'D', 841-1210, 'I', 1212-1383, 1389-2299, 'QM', 2302-2490 <RE2>  
A:Cross-references: GB:D21209; NID:G452189; PIDN:BA04750.1; PID:G452190  
A:Gene: GDB:PTPN13  
A:Cross-references: GDB:306348; OMIM:600267  
A:Map position: 4q21.3-4q21.3  
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology; I  
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosi  
F:574-868/Domain: protein 4.1 membrane-binding domain homology <B41>  
F:1099-1175/Domain: GLGF domain homology <GLG1>  
F:1373-1454/Domain: GLGF domain homology <GLG2>  
F:1511-1590/Domain: GLGF domain homology <GLG3>  
F:1799-1870/Domain: GLGF domain homology <GLG4>  
F:1893-1967/Domain: GLGF domain homology <GLG5>  
F:2242-2461/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F:2413/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:2419/Binding site: substrate phosphate (Arg) #status predicted  
Query Match 28.8%; Score 645; DB 1; Length 2490;  
Best Local Similarity 34.2%; Pred. No. 5.3e-38;  
Matches 147; Conservative 75; Mismatches 152; Indels 56; Gaps 9;  
6 KVRGKTGDRNDEEGNSGNLNRSLP---SSSKMTPTKPIFGNKNSENKVPKSHLSF 62  
2094 KNGKLSERTEDTDCG-----SPLPEYFEATKNGCEYCKEYKSESL----- 2140  
63 SDKYELVYPEFLESDTDTETWVDVDRSLRNWNSMDSETAGPKTSVPLSGSSRLSKDT 122  
2141 -----IQKPEKKTDDDEITWG-NDELPERTNHEDSD-----KD- 2174  
123 ETSVSEKELTQAIQIRPLIFNSSARSAMRDCNLTQ-----KKEELDIIIRRELEQM 175  
2175 HSFLTNDELAVLPVVKVLPSPGKYTGANKLSVIRVLRGLDQGIKPSKELENLQELKPLDQC 2234





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;Date: 01-Mar-1996 #sequence_revision 08-Mar-1996 #text_change 22-Jun-1999
;Accession: I38670; I52599
;Author: Ostman, A.; Yang, Q.; Tonks, N.K.
;J: Natl. Acad. Sci. U.S.A. 91, 9680-9684, 1994
;Title: Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced
;Reference number: I38670; MUID:95024024; PMID:7937872
;Accession: I38670
;Molecule type: mRNA
;Residues: 1-1337 <RES>
;Cross-references: EMBL:U10886; NID:G558754; PID:G558755
;Experimental source: Hela cells
;Honda, H.; Inazawa, J.; Nishida, J.; Yazaki, Y.; Hirai, H.
;Proc Natl Acad Sci USA 91:4194-4199, 1994
;Title: Molecular cloning, characterization, and chromosomal localization of a novel pr
;Reference number: I52599; MUID:95086212; PMID:7994032
;Accession: I52599
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: mRNA
;Residues: 1-216, 'LTVGRKAA', 225-260, 'G', 262-285, 'GTEGGLDASNTSRSA', 302, 'S', 304, 'TAPVHDE
;Cross-references: GB:D37781; NID:G633072; PID:HA007035.1; PID:G633073
;Comment: Enhanced expression of this protein with increasing cell density suggests a r
;Genetics:
;Gene: GDB:PTPRJ
;Cross-references: GDB:385040; OMIM:600925
;Map position: 19q13.4-19q13.4
;Function:
;Description: catalyzes hydrolysis of peptidyl-tyrosine to peptidyl-tyrosine and
;Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III repea
;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor; tran
;1-35/Domain: signal sequence #status predicted <SIG>
;36-1337/Product: protein-tyrosine-phosphatase, receptor type J #status predicted <MAT>
;118-197/Domain: fibronectin type III repeat homology <3FNB>
;206-283/Domain: fibronectin type III repeat homology <3FNB>
;284-356/Domain: fibronectin type III repeat homology <3FNB>
;365-445/Domain: fibronectin type III repeat homology <3FNB>
;453-530/Domain: fibronectin type III repeat homology <3FNB>
;539-617/Domain: fibronectin type III repeat homology <3FNB>
;720-804/Domain: fibronectin type III repeat homology <3FNB>
;972-988/Domain: transmembrane #status predicted <TM>
;1065-1287/Domain: protein-tyrosine-phosphatase homology <PTP>
;72,82,93,104,142,172,231,258,278,342,351,376,391,396,413,431,501,525,536,582,603,6
;1239/Active site: Cys (phosphotyrosine intermediate) #status predicted
;1245/Binding site: substrate phosphate (Arg) #status predicted

Query Match 21.7%; Score 487; DB 1; Length 1337;
Best Local Similarity 34.9%; Pred. No. 6e-27;
Matches 110; Conservative 63; Mismatches 114; Indels 28; Gaps 8;
y 119 SKDTSSVSKELTQLAQRPLIFNSSARSAMDCLNTLQKEELD---IIREPLELEQ 174
b 1003 AKNEVSFS-----QIKP-----KSKLIRVENFPAFFKQQAADNSCGFAEYEDLKL 1050
y 175 MTLPPDDFNSGNTLQNRDKRYRDLIPYDSTRVPLG-----KNKDYINASVIRIVNHEEYFV 230
b 1051 VGISQPKYAAELAEKGRKRYNVLPIYDLSRVKLSVQTHSTDDYINANTPGYHSKD-- 1108
y 231 YIATQGPLPETIEDFWQVLENNCNVAMITREIBCGVIKCYSWPISLKEPLPEHFSV 290
b 1109 FIATQGPLPNTLKDFFWVWEKYNVAILMLTQVEQGRTKCEYNP--SKQAQVDGDTV 1166
y 291 FLTEFWTQYFTRVQIVKSGTGKSCQVKKHLOFTKWDHGTGPSADFFIKY---VR-YV 346
b 1167 AMTSEIVLPWTIRDFTRVKNIQTSSEHPLRQHFHTSWPDHGVDFDTLLINFRYLVRDYM 1226
y 347 RKSHITGPILVHCSAGVGRGVFCVDVVFSAIEKNYSFDIMNIVTQMRKORCGMIQTK 406
b 1227 KQSPSPSPILVHCSAGVGRGVFTIADRLIYQIENENTVDVYGVYDLRMRPLMVQTED 1286
y 407 QYQFCYIEVEVLQN 421.
b 1287 QYVFLNQCVLDIVRS 1301
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```
RESULT 11
S51005
protein-tyrosine-phosphatase (EC 3.1.3.48) 2E - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Apr-1996 #sequence_revision 03-May-1996 #text_change 22-Jun-1999
C;Accession: S51005; S51161
R/L'Abbe, D.; Barville, D.; Tong, Y.; Stocco, R.; Masson, S.; Ma, S.; Fantus, G.; Shen,
FEBS Lett. 356, 351-356, 1994
A;Title: Identification of a novel protein tyrosine phosphatase with sequence homology t
A;Reference number: S51005; MUID:95104449; PMID:7805871
A;Accession: S51005
A;Molecule type: mRNA
A;Residues: 1-1175 <LAA>
A;Cross-references: EMBL:U17971; NID:G662113; PID:AAA62153.1; PID:G6032255
A;Genetics: PTP2E
A;Accession: S51161
A;Molecule type: mRNA
A;Residues: 840-1175 <LAB>
A;Cross-references: EMBL:U18293; NID:G603228; PID:AAA62154.1; PID:G603229
A;Genetics: PTP2E1
A;Genetics: <PTP2E>
A;Note: clone PTP2E
C;Genetics: <PTP2E1>
A;Note: clone PTP2E1
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-b
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
E;25-304/Domain: protein 4.1 membrane-binding domain homology <B41>
F;922-1157/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1109/Active site: Cys (phosphotyrosine intermediate) #status predicted
F;1115/Binding site: substrate phosphate (Arg) #status predicted

Query Match 21.6%; Score 484.5; DB 2; Length 1175;
Best Local Similarity 28.2%; Pred. No. 7.5e-27;
Matches 146; Conservative 69; Mismatches 141; Indels 161; Gaps 17;
Qy 44 IFGNKXNSNVKP-----SHLPSDKYELVYPPLESDDTETVWDVSDSLRNWNSM 97
Db 677 VPSDKVKQEGTBEQSGGYSHKSLSDATMLIH-----SSEEDLDDSSREHAYSE 729
Qy 98 DSETAG-----PSKTVSPV-----LSGSSRLSKD-----TET----- 124
Db 730 PRUTAFSQQQLNYPCASVTPVTPGLHIFPKSHVTFEKKRAKDISPVHLVMETHQPR 789
Qy 125 -----SVSEKELTQLAQRPLIFNSSARSAMDCL-----NTLQ----- 158
Db 790 HGLLTPTSMSESLDITTSGRYR-----ARRDSLKKRPVSDLLSGKKMTVEGLPLOG 839
Qy 159 -KKELDITR-----EFLSQMTLPDDFNSGNTL----- 187
Db 840 MKKTRADAKKIGPLKLAALNGLSLRLPLPDEGKEVSTRAINDERCKVLEQRLQGTWPT 899
Qy 188 -----QNRDKNRYRDLIPYDSTRVPLGKND-----YINASYIRI 222
Db 900 EYERILKXGLVDGECSTARLPENAEENRFQDVLVYDDARVELVPTKENNTGYINASHIKV 959
Qy 223 VNHEBYFYIATQGPLPETIEDFWQVLENNCNVAMITREIBCGVIKCYSWPISLKEP 282
Db 960 SVSGIEWDYIATQGPLQNTQDFWQVWEQGVALLIYVTAEEGGRKSFYWP-----R 1014
Qy 283 LEFEHPSVLETFHVTQYF-----TVRVFQIVKSGTGKSCQVKKHLOFTKWDHGTGPS 335
Db 1015 LGSRNVTYTGFKITTRPTDSGCCVATTGLAKMKELLTGQENTVHLLQYTDWPEHGCPE 1074
Qy 336 ADFFIKYRVY-----RKSHITG-----PLLVHCSAGVGRGVFCVDVVFSAIEKNYS 384
Db 1075 LKGFSLYSEIQSVRHRTNSTSEPSNPPLLVHCSAGVGRGVVILSEIMVACLEHNEV 1134
Qy 385 FDIINIVTQMRKORCGMIQTKQYQFCYIEVEVLQN 421
Db 1135 LDIPRVLELRQORMLVQTLQSQYTFVTRVLIQFLKS 1171

RESULT 12
```

50212  
rotein-tyrosine-phosphatase (EC 3.1.3.48) - Chicken  
;Species: Gallus gallus (chicken)  
;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jan-2000  
;Accession: I50212  
;Stoker, A.W. 201-217, 1994  
;Title: Isoforms of a novel cell adhesion molecule-like protein tyrosine phosphatase and its role in the regulation of cell growth and differentiation  
;Reference number: I50212; MUID:95001563; PMID:7918104  
;Accession: I50212  
;Status: preliminary  
;Molecule type: mRNA  
;Residues: 1-1499 <STO>  
;Cross-references: GB:I32780; NID:9485746; PIDN:AAA64460.1; PID:9485747  
;Gene: CRYPalphal  
;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
SY  
;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
;148-208/Domain: immunoglobulin homology <IMM1>  
;245-299/Domain: immunoglobulin homology <IMM2>  
;881-1499/Domain: fibronectin type III repeat homology <3PR>  
;1257-1479/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
;1141/Active site: Cys (phosphocysteine intermediate) #status predicted  
;1147/Binding site: substrate phosphate (Arg) #status predicted  
;1432/Active site: Cys (phosphocysteine intermediate) #status predicted  
;1438/Binding site: substrate phosphate (Arg) #status predicted  
Query Match 21.6%; Score 483; DB 2; Length 1499;  
Best Local Similarity 38.0%; Pred. No. 1.4e-26;  
Matches 109; Conservative 54; Mismatches 100; Indels 24; Gaps 9;  
Y 151 RCLNTLQKKBELDIREF--LELQMTLPD-----FNSGNTLQNRDKRYRDLIPYD 202  
D 1211 RMLTYIQKLAQIEGHEVHTGKELSEFKRLANSKAHTSRFISANLPCNFKRLNIMKPYE 1270  
I 203 STRVPLG-----KNKDYINASIRIVNHEEYFIATQGLPETIEDFWQVLENNCNVI 257  
D 1271 TRVCLQTRGVGSDYINASFID--GYRQKAYIATQGLPETIEDFWMLWENNSTIV 1328  
Y 258 AMTIREICGVIKCYSYNPISLKEPLHFHSVP--LETFHTVQYFVRVQVIVKSKTGKS 316  
D 1329 VMLTKLRMGREKCHQYWP--AERSARYQYFVVDPAEYNNPQYI-LREFKVTARDGQS 1385  
I 317 QCVKHLQFTWPDHGTTPASADFFIKYRVYRKSH-----ITGPLLHCSAGVGRGTGVCV 372  
D 1386 RTVRQFQFTDWPESQGVKSGEGFIDFQGVHKTKEQFGQDGPISVHCSAGVGRGTGVT 1445  
Y 373 DVVFSALERNYSFDIMNIYVQMRKQRCGMIOQKEQYQFCYIVLEVL 419  
D 1446 SIVLERMYEGVVDIFQTVQMLRTQ--AMVQTEDEYQFCYQAALAYL 1491  
RESULT 13  
rotein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - human  
;Alternate names: protein-tyrosine-phosphatase Bptp-2  
;Species: Homo sapiens (man)  
;Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 21-Jan-2000  
;Accession: A56178; S12052; E44929  
;Fullido, R.; Krueger, N.X.; Serra-Pages, C.; Saito, H.; Streuli, M.  
;Biol. Chem. 270, 6722-6728, 1995  
;Title: Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta isoforms.  
;Reference number: A56178; MUID:95204468; PMID:7896816  
;Accession: A56178  
;Status: preliminary  
;Molecule type: mRNA  
;Residues: 1-1912 <PUL>  
;Cross-references: GB:I38929; NID:9755652; PIDN:AA041749.1; PID:g755653  
;Krueger, N.X.; Streuli, M.; Saito, H.  
;BO J. 9, 3241-3252, 1990  
A;Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatases  
A;Reference number: S12049; MUID:91006018; PMID:2170109  
A;Accession: S12052  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 390-1912 <XRU>  
A;Cross-references: GB:XS4133; NID:935789; PIDN:CAA9068.1; PID:g35790  
A;Note: the sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 568-T  
R;Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, P.; Hinoda, Y.; Imai, K.; Yac  
Cancer Res. 52, 737-740, 1992  
A;Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.  
A;Reference number: A44929; MUID:92119637; PMID:1370651  
A;Accession: B44929  
A;Molecule type: mRNA  
A;Residues: 1756-1804, 'C', 1806-1845 <ADA>  
A;Cross-references: GB:S78086; NID:9243545; PIDN:AA021147.1; PID:g243546  
A;Experimental source: pre-B cell NALM-6  
A;Note: sequence extracted from NCBI backbone (NCBI:78086, NCBIP:78087)  
A;Note: the authors did not report the entire codon for residue 90  
C;Genetics:  
A;Gene: GDB:PTPRD  
A;Cross-references: GDB:131384; OMIM:601598  
A;Map position: 9p24-9p24  
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
OGY  
;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane  
F;38-100/Domain: immunoglobulin homology <IMM1>  
F;140-209/Domain: immunoglobulin homology <IMM2>  
F;250-304/Domain: immunoglobulin homology <IMM3>  
F;711-811/Domain: fibronectin type III repeat homology <3PR>  
F;1293-1912/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F;1669-1892/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F;1553/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;1559/Binding site: substrate phosphate (Arg) #status predicted  
F;1844/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;1850/Binding site: substrate phosphate (Arg) #status predicted  
Query Match 21.5%; Score 481.5; DB 2; Length 1912;  
Best Local Similarity 40.2%; Pred. No. 2.5e-26;  
Matches 107; Conservative 45; Mismatches 99; Indels 21; Gaps 7;  
QY 170 LELEQMTLPD-----FNSGNTLQNRDKRYRDLIPYDSTRVPLG-----KNKDYINAS 218  
DB 1644 MSLEFKRLASSKAHTSRFISANLPCNFKRLNIMPYESTRVCLQTRGVGSDYINAS 1703  
QY 219 YRIVNHEEYFIATQGLPETIEDFWQVLENNCNVIAMTIREICGVIKCYSYWPIS 278  
DB 1704 FID--GYRQKAYIATQGLPETIEDFWMLWENNSTIVVMTKLREMGREKCHQYWP-- 1759  
QY 279 LKEPLEFHFHSVP--LETFHTVQYFVRVQVIVKSKTGKSQCVKHLQFTWPDHGTTPASAD 337  
DB 1760 AERSARYQYFVVDPAEYNNPQYI-LREFKVTARDGQSRVTRVQFQFTDWPESQGVKSGE 1818  
QY 338 FFIKRVYVYRKSH-----ITGPLLHCSAGVGRGTGVCVIVVFSALERNYSFDIMNIYVQ 393  
DB 1819 GFIDFQGVHKTKEQFGQDGPISVHCSAGVGRGTGVTLSIVLERMYEGVVDIFQTVKM 1878  
QY 394 MKQRCGMIOQKEQYQFCYIVLEVL 419  
DB 1879 LITQRPAMVQTEDEYQFCYQAALAYL 1904  
RESULT 14  
I58345  
protein tyrosine phosphatase - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 22-Jun-1999  
C;Accession: I58345  
R;Higashitsuguji, H.; Arii, S.; Furutani, M.; Imamura, M.; Kaneko, Y.; Takeda, J.; Nakay;  
Oncogene 10, 407-414, 1995  
A;Title: Enhanced expression of multiple protein tyrosine phosphatases in the regenerative  
tal protein 4.1.  
A;Reference number: I58345; MUID:95140431; PMID:7838537

Accession: I58345  
;Status: preliminary; translated from GB/EMBL/DBJ  
;Molecule type: mRNA  
;Residues: 1-1176 <RES>  
;Cross-references: GB:D37801; NID:9604885; PIDN:BA07053.1; PID:9604886  
;Genetics:  
;Gene: PTP-RL10  
;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-h  
;Keywords: phosphoprotein  
;25-304/Domain: protein 4.1 membrane-binding domain homology <B41>  
;923-1158/Domain: protein-tyrosine-phosphatase homology <PTP>  
;1110/Active site: Cys (phosphocysteine intermediate) #status predicted  
;1116/Binding site: substrate phosphate (Arg) #status predicted

Query Match 21.5%; Score 481; DB 2; Length 1176;  
Best Local Similarity 28.5%; Pred. No. 1.3e-26;  
Matches 143; Conservative 74; Mismatches 155; Indels 130; Gaps 16;  
Y 44 IFGKNSNSNVK-----SHLSFSDKYELV-----YEPLESDT--DETVDYSDSLR 91  
b 677 VFSCKMKQGTGTEQEGRYSHKLSLSDATWGLDSSEDEEDLESRSQAISAVSEPLT 736  
Y 92 NRWN-----SMDSETAGP-----SKTVPSPV--LSGSSRLSKD--TET 124  
b 737 AAFSOLNYPCASATITGTHIFBPKPHVTPSKRAKDIPVHLVVTETPRRDGLLTP 796  
Y 125 SVSEKELTQAQI-----RPLFNSSARSAMDCLNTL--OKKELEDIR----- 167  
b 797 SMSESLLTSGRYARRDSVKRPVSDLLSGKSAVEGLPLPGGMKTRADAKKIGPLK 856  
Y 168 ---EFILEQMTLPDDFNSGNTL----- 187  
b 857 AALNGLSLSLPLPDGKEVSTRAINDERCKVLEQGMVFTEYERILKKLVDGEC 916  
Y 188 -----ONRDKNRYDILPYDSTRVPLGKXO-----YINASYIRIWNHEEYFYIATQGPL 238  
b 917 TARLPENASERNPDVLPYDDARVELVPTKENNTGYINASHIKVSUSGIEWDYIATQGPL 976  
Y 239 PETIEDFMQWLENNCNVIAMITREIECCVVKYVWPISLKEPLEFHFVSFLETHVT 298  
b 977 QNTCQDFQWVWEOGVAILAMWTABEEGRKSFYWP-----RLGSRHNTVYGRPKIT 1031  
Y 299 QYF-----TVRVFQIVKSKGQCVKHLQFTKWPDHGTTPASADFFIKVRYVR----- 347  
b 1032 TRPRTDGCYATFTGLKQKHLTGQERTVWHLQYTDWPEHGPCPEDLKFLSYLEBISQVR 1091  
Y 348 -----KSHITGPLLKCSAGVGTGVCVDFVFSIAEKYNSFDIMNIYVQMRKQRC 399  
b 1092 HTNSTSEPKSH-NPPELLVHCSAGVGTGTVLLSEIMVACLEHNEVLDPVRLDMLRQRM 1150  
Y 400 GMTQKEQYQFCYEVILEVLQN 421  
b 1151 MLVQTLGQYTFVRYVLIQFLKS 1172

RESULT 15  
53978  
rotein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type PTPX10 - African clawed frog  
;Species: Xenopus laevis (African clawed frog)  
;Date: 25-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 22-Jun-1999  
;Accession: B53978  
;Del Vecchio, R.L.; Tonks, N.K.  
;Biol. Chem. 269, 19639-19645, 1994  
;Title: Characterization of two structurally related Xenopus laevis protein tyrosine ph  
;Reference number: A53978; MUID:94308257; PMID:8034733  
;Accession: B53978  
;Status: preliminary  
;Molecule type: mRNA  
;Residues: 1-597 <DEL>  
;Cross-references: GB:I33099; NID:9495671; PIDN:AAA21728.1; PID:9495672  
;Experimental source: ovary  
;Note: sequence extracted from NCBI backbone (NCBI:149759, NCBI:P:149760)  
;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 9; cellular retinaldehyde-

C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas  
F;38-227/Domain: cellular retinaldehyde-binding protein homology <CRB>  
F;328-564/Domain: protein-tyrosine-phosphatase homology <PTP>  
F;516/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;522/Binding site: substrate phosphate (Arg) #status predicted

Query Match 21.4%; Score 479; DB 2; Length 597;  
Best Local Similarity 35.7%; Pred. No. 6.9e-27;  
Matches 104; Conservative 51; Mismatches 110; Indels 26; Gaps 6;  
QY 152 DCLNTLQKKEELDITREPFLLEQMTLPDDFNSGNTLQNRDKRYRDILPYDSTRVPLG-- 209  
Db 291 DLVQVRRKKKGIGFQYEIEIRKDPVGSFDSKSKHQVRYSDVLCDSRVKLGVLV 350  
QY 210 ---KNKDYINASYIRIWNHEEYFYIATQGPLPETIDFMQWLENNCNVIAMITREIEC 266  
Db 351 GTDETTDYINASFMD--GYKRKNVAVIATQGPLKTFDDFRWVWQKVLIIWMTTRVIER 408  
QY 267 GVTKCYSVNPISLKEPLEFHFVSFLETHVT--QYFTVRVFIKSKSGKSCQVKHLQF 324  
Db 409 GRICKCQYWPLEAGRSEDUTGHF--IIRNIHIDLPODKLTFEVTNKQIDESRSVAHTQY 466  
QY 325 TKWPDHGTTPASADFFIKVRYVRK-----SHITG-ELLVHCSAGVGTGTF 369  
Db 467 MSWPDGFGVFKSASAMLDPRSQVQKQAVAVQNLGMWGTGHPAGPPIVHCSAGIGRTGTF 526  
QY 370 ICVDVVFSAIEKNYSFDIMNIYVQMRKQRCGMIOYKQYQFCYEVILEVLQ 420  
Db 527 CTLDICLSLEDIGTVVDVLQTVKRMRTQASFSIQTWQYFYFCYMAIIIEYAO 577

Search completed: June 16, 2004, 13:24:52  
Job time : 22 secs



GenCore version 5.1.6  
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1 protein - protein search, using sw model

on on: June 16, 2004, 13:16:50 ; Search time 17 Seconds  
(without alignments)  
1304.817 Million cell updates/sec

file: US-09-095-478A-5

Effect score: 2241

Sequence: 1 MSSPRKVRGKTGRNDDEEG.....QYQFCYEIVLEVLQNLALY 426

oring table: BLOSUM62  
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tal number of hits satisfying chosen parameters: 141681

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imum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase : SwissProt\_42\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

sult No.	Score	Query Match	Length	ID	Description
1	653	29.1	2485	1 PTND_HUMAN	Q12923 homo sapien
2	522.5	23.3	1187	1 PTNE_HUMAN	Q15678 homo sapien
3	506	22.6	913	1 PTN3_HUMAN	P26045 homo sapien
4	500	22.3	1189	1 PTNE_MOUSE	O62130 mus musculus
5	496.5	22.2	1948	1 PTNS_HUMAN	Q13332 homo sapien
6	487	21.7	1337	1 PTPJ_HUMAN	Q12913 homo sapien
7	484.5	21.6	1175	1 PTNL_RAT	O62728 rattus norv
8	481.5	21.5	1912	1 PTPD_HUMAN	P23468 homo sapien
9	481	21.5	1176	1 PTNL_MOUSE	Q62136 mus musculus
10	478.5	21.4	926	1 PTN4_HUMAN	P29074 homo sapien
11	477.5	21.3	1454	1 PTPJ_MOUSE	Q9980 mus musculus
12	477	21.3	1463	1 PTPJ_HUMAN	Q14522 homo sapien
13	477	21.3	1997	1 PTPB_HUMAN	P23467 homo sapien
14	475	21.2	1174	1 PTPJ_HUMAN	Q16825 homo sapien
15	475	21.2	1238	1 PTPJ_MOUSE	O64455 mus musculus
16	470	21.0	2316	1 PTPJ_RAT	Q62856 rattus norv
17	469	20.9	1439	1 PTPK_HUMAN	Q15262 homo sapien
18	469	20.9	1452	1 PTPK_HUMAN	P28827 homo sapien
19	468	20.9	1457	1 PTPK_MOUSE	P35822 mus musculus
20	467.5	20.9	1897	1 PTPF_HUMAN	P10566 homo sapien
21	467	20.8	1452	1 PTPM_MOUSE	P28828 mus musculus
22	467	20.8	2314	1 PTPJ_HUMAN	P23471 homo sapien
23	466.5	20.8	415	1 PTN2_HUMAN	P17706 homo sapien
24	466	20.8	377	1 PTP2_DICDI	P34138 dictyostell
25	462	20.6	1216	1 PTPQ_HUMAN	Q16827 homo sapien
26	461	20.6	382	1 PTN2_MOUSE	Q06180 mus musculus
27	459	20.5	363	1 PTN2_RAT	P35233 rattus norv
28	457	20.4	1255	1 CD45_RAT	P04157 rattus norv
29	456	20.3	780	1 PTNC_HUMAN	Q05209 homo sapien
30	456	20.3	2200	1 LAR_CAEBL	Q9bmb caenorhabdi
31	452.5	20.2	360	1 PTN7_HUMAN	P15236 homo sapien
32	451.5	20.1	434	1 PTN1_CHICK	Q13016 gallus gall
33	450	20.1	1152	1 CD45_MOUSE	P06800 mus musculus

RESULT 1	PTND_HUMAN	STANDARD;	PRT; 2485 AA.
AC	Q12923; Q15159; Q15263; Q15264; Q15265; Q15674; Q16826; Q81WH7;		
AC	Q9NTN9;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Protein tyrosine phosphatase, non-receptor type 13 (BC 3.1.3.48)		
DE	(protein-tyrosine phosphatase 1E) (PTP-S1) (hTPPE1) (PTP-BAS);		
DE	(protein-tyrosine phosphatase PTP11) (Fas-associated protein-tyrosine phosphatase 1) (FAP-1).		
GN	PTPN13 OR PTP1E OR PTP1 OR PNP1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM 4).		
RC	TISSUE=Breast carcinoma;		
RX	MEDLINE=94350988; PubMed=8071359;		
RA	Banville D., Ahmad S., Stocco R., Shen S.-H.;		
RT	"A novel protein-tyrosine phosphatase with homology to both the cytoskeletal proteins of the band 4.1 family and junction-associated guanylate kinases.";		
RL	J. Biol. Chem. 269:22320-22327(1994).		
RN	[2]		
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.		
RC	TISSUE=Leukemia;		
RX	MEDLINE=94116679; PubMed=8287977;		
RA	Maekawa K., Imagawa N., Nagamatsu M., Harada S.;		
RT	"Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane-binding domain and GLGF repeats.";		
RL	FEBS Lett. 337:200-206(1994).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Fibroblast;		
RX	MEDLINE=95014139; PubMed=7929060;		
RA	Saras J., Claesson-Welsh L., Heldin C.-H., Gonez L.J.;		
RT	"Cloning and characterization of PTP11, a protein tyrosine phosphatase with similarities to cytoskeletal-associated proteins.";		
RL	J. Biol. Chem. 269:24082-24089(1994).		
RN	[4]		
RP	SEQUENCE OF 1216-2490 FROM N.A.		
RC	TISSUE=Pancreas;		
RA	Wang H.Y.;		
RL	Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.		
RN	[5]		
RP	SEQUENCE OF 1279-1883 FROM N.A. (ISOFORM 4).		
RC	TISSUE=Brain;		
RX	MEDLINE=95232528; PubMed=7536343;		
RA	Sato T., Irie S., Kitada S., Reed J.C.;		
RT	"FAP-1: a protein tyrosine phosphatase that associates with Fas.";		
RL	Science 268:411-415(1995).		
RN	[6]		
RP	SEQUENCE OF 1323-1821 FROM N.A.		

P16621 drosophila  
P35831 mus musculus  
P23470 homo sapien  
P28191 caenorhabdi  
P08575 homo sapien  
P18031 homo sapien  
P49445 rattus norv  
P20417 rattus norv  
P43378 homo sapien  
P35821 mus musculus  
Q90687 gallus gall  
P41499 rattus norv

#### ALIGNMENTS

Irie S., Hachiya T., Sato T.A.;  
Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
[7]  
SEQUENCE OF 1323-1922 FROM N.A.  
TISSUE=Eye;  
MEDLINE=2238857; PubMed=12477932;  
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
A Altschul S.F., Zdobych B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
A Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,  
A Brownstein M.J., Udell T.B., Toshiyuki S., Cantinci P., Prange C.,  
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
A Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W.,  
A Villalón D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
A Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
A Whiting M., Madan A., Young A.C., Shevchenko Y., Souffard G.G.,  
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[8]  
INTERACTION WITH TRIP6.  
MEDLINE=93329089; PubMed=10400701;  
A Murthy K.K., Clark K., Fortin Y., Shen S.-H., Banville D.;  
"ZRP-1, a zyxin-related protein, interacts with the second PDZ domain  
of the cytosolic protein tyrosine phosphatase hPTP1E";  
J. Biol. Chem. 274:20679-20687 (1999).  
[9]  
INTERACTION WITH NGFR.  
MEDLINE=20012928; PubMed=10544233;  
A Irie S., Hachiya T., Rabizadeh S., Maruyama W., Mukai J., Li Y.,  
A Reed J.C., Bredesen D.E., Sato T.A.;  
"Functional interaction of Fas-associated phosphatase-1 (FAP-1) with  
p75 (NTR) and their effect on NF-kappaB activation";  
FEBS Lett. 460:191-198 (1999).  
[10]  
STRUCTURE BY NMR OF 1361-1456 UNCOMPLEXED AND IN COMPLEX WITH THE  
C-TERMINUS OF TNFRSF6.  
MEDLINE=20170882; PubMed=10704206;  
A Kozlov G., Gehring K., Ekkel I.;  
"Solution structure of the PDZ2 domain from human phosphatase hPTP1E  
and its interactions with C-terminal peptides from the Fas  
receptor";  
Biochemistry 39:2572-2580 (2000).  
[11]  
STRUCTURE BY NMR OF 1361-1456 IN COMPLEX WITH THE C-TERMINUS OF THE  
GUANINE NUCLEOTIDE EXCHANGE FACTOR RA-GEF-2.  
MEDLINE=22090786; PubMed=12095257;  
A Kozlov G., Banville D., Gehring K., Ekkel I.;  
"Solution structure of the PDZ2 domain from cytosolic human  
phosphatase hPTP1E complexed with a peptide reveals contribution of  
the beta2-beta3 loop to PDZ domain-ligand interactions";  
J. Mol. Biol. 320:813-820 (2002).  
[12]  
VARIANTS PRO-1419 AND MET-1522.  
MEDLINE=22323362; PubMed=12436199;  
A Yoshida S., Harada H., Nagai H., Fukino K., Teramoto A., Emi M.;  
"Head-to-head juxtaposition of Fas-associated phosphatase-1 (FAP-1)  
and c-Jun NH2-terminal kinase 3 (JNK3) genes: genomic structure and  
seven polymorphisms of the FAP-1 gene";  
J. Hum. Genet. 47:614-619 (2002).  
[13]  
FUNCTION: Regulates negatively Fas-induced apoptosis and NGFR-  
mediated pro-apoptotic signaling.  
[14]  
CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
tyrosine + phosphate.  
[15]  
SUBUNIT: Interacts with TRIP6 and TNFRSF6 (Fas receptor) through  
its second PDZ domain. Interacts with the C-terminal SVP motif of

NGFR through its third PDZ domain.  
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
ALTERNATIVE PRODUCTS:  
Event-Alternative splicing; Named isoforms=4;  
Name=1;  
IsoId=Q12923-1; Sequence=Displayed;  
Name=2;  
IsoId=Q12923-2; Sequence=VSP\_000496;  
Name=3;  
IsoId=Q12923-3; Sequence=VSP\_000497;  
Name=4;  
IsoId=Q12923-4; Sequence=VSP\_007921;  
Note=May be due to a competing donor splice site;  
TISSUE SPECIFICITY: Present in most tissues with the exception of  
the liver and skeletal muscle. Most abundant in lung, kidney and  
fetal brain.  
[16]  
SIMILARITY: Contains 1 FERM domain.  
[17]  
SIMILARITY: Contains 5 PDZ/DRH domains.  
[18]  
SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
Non-receptor class subfamily.  
[19]  
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[20]  
EMBL: U12128; BAB60339.1; -  
EMBL: D21209; BAA04750.1; -  
EMBL: D21210; BAA04751.1; -  
EMBL: D21211; BAA04752.1; -  
EMBL: X80289; CAA56563.1; -  
EMBL: X79676; CAA56124.1; -  
EMBL: I34583; AAC1755.1; -  
EMBL: AP233323; AAF63474.1; -  
EMBL: BC039610; AAF39610.1; ALT\_TERM.  
PIR: A54971; A54971.  
PIR: I67623; I67623.  
PIR: I67630; I67630.  
PDB: 3PDZ; 17-MAR-00.  
PDB: 1DSG; 24-JUL-02.  
GeneW: HGNC:9646; PTPN13.  
MIM: 600267; -  
GO: GO:0004725; P:protein tyrosine phosphatase activity; TAS.  
GO: GO:000470; P:protein amino acid dephosphorylation; TAS.  
InterPro: IPR000299; Band\_4.1.  
InterPro: IPR001478; PDZ.  
InterPro: IPR00387; TYR phosphatase.  
Pfam: PF00373; Band 41; 1.  
Pfam: PF00595; PDZ\_5.  
PRINTS: PR00935; BAND41.  
PRINTS: PR00700; PTPPHPTASE.  
SMART: SM00295; B41; 1.  
SMART: SM00288; PDZ; 5.  
SMART: SM00194; PTPC; 1.  
PROSITE: PS00660; FERM\_1; FALSE\_NEG.  
PROSITE: PS00661; FERM\_2; FALSE\_NEG.  
PROSITE: PS00507; FERM\_3; 1.  
PROSITE: PS0106; PDZ; 5.  
PROSITE: PS00383; TYR PHOSPHATASE 2; 1.  
PROSITE: PS00556; TYR PHOSPHATASE 1; FALSE\_NEG.  
PROSITE: PS00555; TYR PHOSPHATASE 2; 1.  
Structural protein; Cytoskeleton; Coiled coil; Polymorphism.  
Alternative splicing; Coiled coil; Polymorphism.  
DOMAIN 56 59  
DOMAIN 572 572  
DOMAIN 2237 2485  
DOMAIN 379 399  
DOMAIN 469 504  
PROTEIN-TYROSINE PHOSPHATASE.  
COILED COIL (POTENTIAL).  
COILED COIL (POTENTIAL).





X NCBI\_TaxID=10090;  
 N [1]  
 P SEQUENCE FROM N.A. TISSUE=Thymus;  
 C STRAIN=CB-17-SCID; PubMed=8074693;  
 X MEDLINE=94354845; PubMed=8074693;  
 X Sawada M., Ogata M., Fujino Y., Hamaoka T.;  
 T "cDNA cloning of a novel protein tyrosine phosphatase with homology  
 I to cytoskeletal protein 4.1 and its expression in T-lineage cells.";  
 L Biochem Biophys Res Commun. 203:479-484(1994).  
 C -!- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF T CELL DEVELOPMENT.  
 C -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2O) = protein  
 C tyrosine + phosphate.  
 C -!- TISSUE SPECIFICITY: Thymus; in cells of both hematopoietic and  
 C non-hematopoietic origins.  
 C -!- SIMILARITY: Contains 1 FERM domain.  
 C -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
 C Non-receptor class subfamily.  
 C  
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 C or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 C  
 C EMBL; D31842; BAA0628.1; --  
 C PIR; JC2366; JC2366.  
 C HSSP; O06124; 2SHP.  
 C WGD; MG1:102467; Ecpn14.  
 C InterPro; IPR000299; Band 4.1.  
 C InterPro; IPR000387; Tyr\_phosphatase.  
 C InterPro; IPR000242; Tyr\_PP.  
 C Pfam; PF00373; Band 4.1.  
 C Pfam; PF00102; Y\_phosphatase; 1.  
 C PRINTS; PR00935; BAND41  
 C PRINTS; PR00700; PRTYPHPTASE.  
 C SMART; SM00295; B41; 1.  
 C SMART; SM00194; PTPC; 1.  
 C PROSITE; PS00660; FERM 1; 1.  
 C PROSITE; PS00661; FERM 2; 1.  
 C PROSITE; PS00057; FERM 3; 1.  
 C PROSITE; PS00383; TYR\_PHOSPHATASE 1; 1.  
 C PROSITE; PS00555; TYR\_PHOSPHATASE\_PTP; 1.  
 C PROSITE; PS00556; TYR\_PHOSPHATASE 2; 1.  
 C Structural protein; Cytoskeleton; Hydrolase.  
 C DOMAIN 21 306 FERM.  
 C ACT\_SITE 1123 1123  
 C DOMAIN 566 573 POLY-PRO.  
 C DOMAIN 635 639 POLY-GLY.  
 C DOMAIN 712 718 POLY-GLU.  
 C SEQUENCE 1189 AA; 135030 MW; 2B85BE5F9C723303 CRC64;  
 Query Match 22.3%; Score 500; DB 1; Length 1189;  
 Best Local Similarity 27.0%; Pred. No. 8e-27;  
 Matches 153; Conservative 79; Mismatches 153; Indels 182; Gaps 18;  
 Y 20 GNSGNLNR-----NSLPSSQKMT-----PTKPIFGNKNSENK 55  
 b 636 GGGGTGKRSLSLVNMSVGRMEAMTKSLNTPMARRNTLREQGSRBTGHEVHG---L 692  
 Y 56 PSHH--LSESDKVELVYPPLSDTDETVWDSR-----SLRNKNSM 97  
 b 693 PQVHKKTSTMTLHSS--SSEBEEETLEAPQVPLREKVBYSALQAALAIRNP 750  
 Y 98 DSFTAGFSTVPSVLSGSRSLSKDTE----- 123  
 b 751 PPEYPCPRKSVS---NGALRQDQGTPLPAMRCVLRHGHGSKALSVSAEQLVNGLS 807  
 Y 124 TVSVSEKLTQL-----AQTRPL 140  
 }:::|:::|

Db 808 PSISEPDLTSVKERVKPEVKERFVSEMPSLSDSIIRERMIRNLEKQKMTGQQAQKRLP 867  
 Qy 141 IF-----NSSARSAMRDLNLTQKRELDIIRFLELEQMTLPDD-- 180  
 Db 868 MLAALNGLSVARVSGREDGHDATVPIDRLALKKLEDCGW--FTEYEQ--IPNKA 923  
 Qy 181 ---FNSGNTLQNRNRYEDILPYDSTRVPL---GKNQYINASVIRIVNHEEVEVIA 233  
 Db 924 NGVFTSTATPEAERSRIREVVFTEENRVLLPTKENTGYINASHIKVVVGSGSWHTIA 983  
 Qy 234 TQGLPLETTEDFWQVLENNCNVIMITREIBCGVIKCYSWYPISLKEPLEPEHFSVLE 293  
 Db 984 TQGLPLETCHDFWQVWEQGVAVIAVMTAEBSGRTKSHRYW-----KLSKHS SATVG 1038  
 Qy 294 TEHYTQYF-----TVRFQIVKSTGSKVCKHLOFTKWDHGTPTASADFFIKY---- 342  
 Db 1039 KFKVTTKFTDSCGVATTGLKHLKLLSGOERTVHLQYTDWPHHGCPEDEVQGLFSLBEI 1098  
 Qy 343 --VRYVRKSHITG-----PLVHCSAGVGRGVFICVDVWVPSAIEKQNSFOIMNIVTQM 394  
 Db 1099 QSVRRHTNSVLEGIRTRHPPIVHCSAGVGRGVVLSLSELMYCLERKEVETPLRL 1158  
 Qy 395 RKORCGMIOTKEQYQFCYEVLEVLQN 421  
 Db 1159 REQRMFMQITQYKRYFVYQVLYQLQN 1185  
 RESULT 5  
 PTNS\_HUMAN  
 ID PTNS\_HUMAN STANDARD; PRT; 1948 AA.  
 AC Q1332; Q15718; Q16341;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Receptor-type protein-tyrosine phosphatase S precursor (EC 3.1.3.48)  
 DE (R-PTP-S) (Protein-tyrosine phosphatase sigma) (R-PTP-sigma).  
 GN PTPRS.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Fetal brain;  
 RX MEDLINE=96102179; PubMed=8524829;  
 RA Pulido R., Serra-Pages C., Tang M., Streuli M.;  
 RT "The LAR/PTP delta/PTP sigma subfamily of transmembrane protein-  
 RT tyrosine-phosphatases: multiple human LAR, PTP delta, and PTP sigma  
 RT isoforms are expressed in a tissue-specific manner and associate with  
 RT the LAR-interacting protein LIP-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:11686-11690(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9625038; PubMed=8992885;  
 RA Endo N., Rutledge S.J., Opas E.E., Vogel R., Rodan G.A., Schmidt A.;  
 RT "Human protein tyrosine phosphatase-sigma: alternative splicing and  
 RT inhibition by bisphosphonates.";  
 RL J. Bone Miner. Res. 11:535-543(1996).  
 RN [3]  
 RP SEQUENCE OF 1-126 FROM N.A.  
 RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,  
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,  
 RA Phan H., Velasco N., Do L., Regala M., Terry A., Ganes J., Liu S.,  
 RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,  
 RA Attix C., Andreise T., Frankheim M., Amico-Keller G., Cosfield J.,  
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,  
 RA Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,  
 RA Olsen A.S., Carrano A.V.;  
 RT "Sequence analysis of a 2.5 Mb region in 19p13.3.";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1503-1589 FROM N.A.  
 RX MEDLINE=92119637; PubMed=1370651;

Adachi M., Sekiya M., Arimura Y., Takekawa M., Itoh P., Hinoda Y.,  
Imai K., Yachi A.;  
"Protein-tyrosine phosphatase expression in pre-B cell NALM-6";  
Cancer Res. 52:737-740(1992).  
X C -!- FUNCTION: Interacts with LAR-interacting protein LIP.1.  
X C -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
X C tyrosine + phosphate.  
X C -!- SUBCELLULAR LOCATION: Type I membrane protein.  
X C -!- ALTERNATIVE PRODUCTS:  
X C Event=Alternative splicing; Named isoforms=5;  
X C Comment=Additional isoforms seem to exist;  
X C Name=PTPS;  
X C IsoId=Q13332-1; Sequence=Displayed;  
X C Name=PTPS-MEA;  
X C IsoId=Q13332-2; Sequence=VSP\_050021;  
X C Name=PTPS-MEB;  
X C IsoId=Q13332-3; Sequence=VSP\_050022, VSP\_050026, VSP\_050027;  
X C Name=PTPS-MEC;  
X C IsoId=Q13332-4; Sequence=VSP\_050024;  
X C Name=PTPS-F4-7;  
X C IsoId=Q13332-5; Sequence=VSP\_050023, VSP\_050025;  
X C -!- TISSUE SPECIFICITY: Detected in all tissues tested except for  
X C placenta and liver.  
X C -!- SIMILARITY: BELONGS TO THE RECEPTOR CLASS OF THE PROTEIN-TYROSINE  
X C PHOSPHATASE FAMILY.  
X C -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domain.  
X C -!- SIMILARITY: Contains 8 fibronectin type III domains.  
X C -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
X C -----  
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X C or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
X C -----  
X C EMBL: U35234; AAC50299.1; --  
X C EMBL: U40317; AAC50567.1; --  
X C EMBL: AC005790; AAC62832.1; --  
X C EMBL: S78080; AAB21146.2; --  
X C HSP: P18052; IYFO.  
X C Genew: HGNC:9681; PTPRS.  
X C MIM: 601576; --  
X C GO: GO:0005887; C=Integral to plasma membrane; TAS.  
X C GO: GO:0005001; P=Transmembrane receptor protein tyrosine pho. . .; TAS.  
X C InterPro: IPR008957; FN-III-like.  
X C InterPro: IPR003961; FN-III.  
X C InterPro: IPR003962; FNIII\_subd.  
X C InterPro: IPR007110; Ig-like.  
X C InterPro: IPR003598; Ig C2.  
X C InterPro: IPR000387; Tyr phosphatase.  
X C InterPro: IPR00242; Tyr\_PP.  
X C Pfam: PF00041; fn3; 8.  
X C Pfam: PF00047; Ig; 3.  
X C PRINTS: PF00102; Y\_phosphatase; 2.  
X C PRINTS: PR00014; FNTYPEIII.  
X C PRINTS: PR00700; PTPY\_PHTASE.  
X C SMART: SM00060; FN3; 7.  
X C SMART: SM00408; IG2; 3.  
X C SMART: SM00194; PTPC; 2.  
X C PROSITE: PS50835; IG\_LIKE; 3.  
X C PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
X C PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 2.  
X C PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
X C Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;  
X C Cell adhesion; Immunoglobulin domain; Alternative splicing; Repeat.  
X C SIGNAL 1 25 POTENTIAL.  
X C CHAIN 30 1948 RECEPTOR-TYPE PROTEIN-TYROSINE  
X C PHOSPHATASE S.  
X C DOMAIN 30 1282 EXTRACELLULAR (POTENTIAL).  
X C TRANSMEM 1283 1303 POTENTIAL.  
X C DOMAIN 1304 1948 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 33 123 IG-LIKE C2-TYPE 1.  
FT DOMAIN 135 233 IG-LIKE C2-TYPE 2.  
FT DOMAIN 245 327 IG-LIKE C2-TYPE 3.  
FT DOMAIN 329 423 FIBRONECTIN TYPE-III 1.  
FT DOMAIN 426 522 FIBRONECTIN TYPE-III 2.  
FT DOMAIN 525 615 FIBRONECTIN TYPE-III 3.  
FT DOMAIN 618 717 FIBRONECTIN TYPE-III 4.  
FT DOMAIN 720 831 FIBRONECTIN TYPE-III 5.  
FT DOMAIN 834 926 FIBRONECTIN TYPE-III 6.  
FT DOMAIN 928 1033 FIBRONECTIN TYPE-III 7.  
FT DOMAIN 1036 1151 FIBRONECTIN TYPE-III 8.  
FT DOMAIN 1393 1648 PROTEIN-TYROSINE PHOSPHATASE 1.  
FT DOMAIN 1680 1930 PROTEIN-TYROSINE PHOSPHATASE 2.  
FT DOMAIN 641 644 POLY-PRO.  
FT DISULFID 54 107 POTENTIAL.  
FT DISULFID 156 216 POTENTIAL.  
FT ACT\_SITE 266 311 PHOSPHOCYSTEINE INTERMEDIATE (BY  
FT ACT\_SITE 1589 1589 SIMILARITY).  
FT ACT\_SITE 1880 1880 PHOSPHOCYSTEINE INTERMEDIATE (BY  
FT ACT\_SITE 263 263 SIMILARITY).  
FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 733 733 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 940 940 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPLIC 190 198 Missing (in isoform PTPS-MEA).  
FT VARSPLIC 236 239 Missing (in isoform PTPS-MEB).  
FT VARSPLIC 617 1034 Missing (in isoform PTPS-F4-7).  
FT VARSPLIC 784 792 Missing (in isoform PTPS-MEC).  
FT VARSPLIC 1035 1035 V -> I (in isoform PTPS-F4-7).  
FT VARSPLIC 1350 1365 Missing (in isoform PTPS-MEB).  
FT VARSPLIC 1366 1366 S -> G (in isoform PTPS-MEB).  
FT CONFLICT 310 310 T -> HP (IN REF. 2).  
FT CONFLICT 428 429 SA -> RP (IN REF. 2).  
FT CONFLICT 742 745 LGPV -> RSPA (IN REF. 2).  
FT CONFLICT 765 773 GAGRGPPR -> RREARRRS (IN REF. 2).  
FT CONFLICT 910 910 R -> P (IN REF. 2).  
FT CONFLICT 986 995 AAPGAENAV -> GRLSRRRTL (IN REF. 2).  
FT CONFLICT 1195 1196 TV -> SL (IN REF. 2).  
FT CONFLICT 1431 1431 E -> S (IN REF. 2).  
FT CONFLICT 1546 1546 E -> D (IN REF. 4).  
FT CONFLICT 1587 1587 V -> A (IN REF. 4).  
FT CONFLICT 1705 1705 N -> K (IN REF. 2).  
SQ SEQUENCE 1948 AA; 217080 MW; 7DC049EC03171136 CRC64;  
  
Query Match 22.2%; Score 496.5; DB 1; Length 1948;  
Best Local Similarity 40.6%; Pred. No. 2.7e-26;  
Matches 108; Conservative 47; Mismatches 90; Indels 21; Gaps 7;  
  
Qy 170 LELEQMTLPDD-----FNSGNTLQNRDNRYRDLIPYDSTRVPLG-----KKKDYINAS 218  
Db 1680 MELFKELANSKAHTSRFTISANLPCKNKNLWNTMPYESTRVCLOPIRGVSGSDYINAS 1739  
Qy 219 YIRIVNHEEYPIATOGPIETIEDFQWVLENNCNVIMITREICGVKICYSWPIS 278  
Db 1740 FID--GYROQKAYIATOGPIETIEDFQWVLENNCNVIMITREICGVKICYSWPIS 1795  
Qy 279 LKEPLSEFHFSPV-LETFHVTVTVTVRVPQIVKIGSTGKSCQVKKLQFTKWPDHGTPASAD 337  
Db 1796 AERSARYQVYVDPMAEYVNPQVI-LRBEFKVTARDGGQSRVTRQFQIDWPQGVKPSGE 1854  
Qy 338 PTKYRYRYRKHSH-----ITGPLLHVCAGVGTGTYICVDVVPFSALEKNYSFDINIVTQ 393  
Db 1855 GFIDFTGQVHKTKEQFGQDGPISVHCAGVGTGTYICVDVVPFSALEKNYSFDINIVTQ 1914  
Qy 394 MRKORCGMIQTKEQYQFCYEIVLEVL 419









Query Match 21.5%; Score 481.5; DB 1; Length 1912;  
Best Local Similarity 40.2%; Pred. No. 2.8e-25;  
Matches 107; Conservative 45; Mismatches 93; Indels 21; Gaps 7;  
Y 170 LELEQMTLPDD-----FNSGNTLQNRVDRDLPDSTRVPLG-----KNKDYINAS 218  
b 1644 MELEFRLASSKAHTSRFTSANLPCKNFKNRLVIMPVSTRVCLQPIRGVSGSYINAS 1703  
Y 219 YIIVNHEEYFYATQGPLPETIEDFQWMLNENCNVAMITREIBGCVKCYSYNPIS 278  
b 1704 PID-GYRQKAYATQGLAETTFEWMLEHNSSTVWLTKLRNGREKCHQYWP-- 1759  
Y 279 LKLEPLFEHSPV-LETFHTQYFTVRVQIVKSTGKSCQVHLOFTKWDHGTTPASAD 337  
b 1760 AERSARYQYFVVDMAEYVNPQVI-LREFKVTDAEDGQSRVTRQFQTDWPEQGVPSKSE 1818  
Y 338 FFYKYRVYRKSH---ITGPIVHCSAGVGTGFCVVDVFSIAEKNSYFDMNIVTQ 393  
b 1819 GFIDFICQVHKTEQGGQGPISVHCSAGVGTGFTILSVLEMRVETGVVDIFQIVKM 1878  
Y 394 MKQRCCMIQTEQYQCYEIVLEVL 419  
b 1879 LRTQRPAMVQTEQYQFYSYRAALEVL 1904  
RESULT 9  
TNL\_MOUSE STANDARD; PRT; 1176 AA.  
D PTNL\_MOUSE  
C Q62136;  
T 01-NOV-1997 (Rel. 35, Created)  
T 10-NOV-1997 (Rel. 35, Last sequence update)  
T 10-OCT-2003 (Rel. 42, Last annotation update)  
E Protein tyrosine phosphatase, non-receptor type 21 (EC 3.1.3.48)  
E {protein-tyrosine phosphatase PTP-RL10}.  
N PTPN21.  
S Mus musculus (Mouse).  
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
X NCBI\_TaxID=10090;  
X [1]  
P SEQUENCE FROM N.A.  
C STRAIN=C57BL/6; TISSUE=Liver;  
C MEDLINE=95140431; PubMed=738537;  
A Higashitsuji H., Arii S., Furutani M., Imamura M., Kaneko Y.,  
A Takenawa J., Nakayama H., Fujita J.;  
T "Enhanced expression of multiple protein tyrosine phosphatases in the  
regenerating mouse liver: isolation of PTP-RL10, a novel cytoplasmic-  
type phosphatase with sequence homology to cytoskeletal protein  
4.1.1";  
L Oncogene 10:407-414(1995).  
C -1- FUNCTION: May be involved in the regulation of growth and  
differentiation of liver cells.  
C -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
tyrosine + phosphate.  
C -1- TISSUE SPECIFICITY: Liver.  
C -1- SIMILARITY: Contains 1 FERM domain.  
C -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
C Non-receptor class subfamily.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
C -----  
R EMBL: D37801; BAA07053.1; --  
R PIR: I58345; I58345.  
R R HSSP: P29350; IGWZ.  
R MGD: MGI:1344406; Ptpn21.  
R InterPro: IPR000299; Band 4.1.  
R InterPro: IPR000387; TYR\_phosphatase.

DR InterPro: IPR000242; TYR\_PP.  
DR Pfam: PF00373; Band 41; 1.  
DR Pfam: PF00102; Y\_phosphatase; 1.  
DR PRINTS: PRO0935; BAND41  
DR PRINTS: PRO0700; PRTYPHPTASE.  
DR SMART: SM00295; B41; 1.  
DR SMART: SM00194; PTPC; 1.  
DR PROSITE: PS00660; FERM\_1; 1.  
DR PROSITE: PS00661; FERM\_2; 1.  
DR PROSITE: PS0057; FERM\_3; 1.  
DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
DR PROSITE: PS0055; TYR\_PHOSPHATASE\_PTP; 1.  
DR PROSITE: PS0056; TYR\_PHOSPHATASE\_2; 1.  
KW Structural protein; Cytoskeleton; Hydrolase.  
FT DOMAIN 23 308 FERM.  
FT DOMAIN 923 1176 PROPHOCYSTEINE INTERMEDIATE  
FT ACT\_SITE 1110 1110 (BY SIMILARITY).  
FT DOMAIN 340 343 POLY-PRO.  
FT DOMAIN 565 572 POLY-PRO.  
SQ SEQUENCE 1176 AA; 133490 MW; 529FBE22F1335B75 CRC64;  
Query Match 21.5%; Score 481; DB 1; Length 1176;  
Best Local Similarity 28.5%; Pred. No. 1.6e-25;  
Matches 143; Conservative 74; Mismatches 155; Indels 130; Gaps 16;  
QY 44 IFGNKRNSENVRP-----SHLSFSDKVELV-----YFPLESDT--DETWDVSDRSER 91  
Db 677 VFSDKMKQEGTEQEGRYSHKKSLSDATMLIDSSDEDEDESSRQQAISAVSEPELT 736  
QY 92 NRWN-----SMDSETAGP-----SKTVSPV--LSGSSRLSKD--TET 124  
Db 737 AAFSQELNYPASATPITGPHPEPKHVTPEKRAKDISPVHLVVTHTPRRDLITP 796  
QY 125 SVSEKELTQIAQI-----RPLIFNSSARSAMRDCLNTL--QKGELOIIR----- 167  
Db 797 SMSESOLTTSGRYARRDSVKRPVSDLLSGKSAVEGLPPLGGMKTRADAKKIGPLK 856  
QY 168 ---EPLLEQMTLPDDFNSGNTL-----  
Db 857 AALNGULSLRLPDEGKEVSTRATNDECKVLEORLQSGHVFTEYERILKKELVDGCS 916  
QY 188 -----QNRDKNRYRDLIPYDSTRVPLGKNK-----YINASYIRIVNHEEYFYATQGPL 238  
Db 917 TARTPENARNRFDVLPYDDARVELNPTKNNTGYINASHIKVSVSGIEWDIATQGPL 976  
QY 239 PETIEDFQWMLNENCNVAMITREIBGCVKCYSYWPISLKEPLEFEHSPVLETHVT 298  
Db 977 QNTCDFQWQVWVEQGVAILIAMVTABEGGREGSKFRYP-----RLGSRHNTVYGRFKIT 1031  
QY 299 QYF-----TVRVFQIVKSTGKSCQVHLOFTKWDHGTTPASADFFIKYRVYVR----- 347  
Db 1032 TRFTDSGCVATTGLKMKHLLTQERTVWHLQYTDWPEHGCPEDLKGFLSYLEIQSVRR 1091  
QY 348 -----KSHITGPLLHCSAGVGTGFCVVDVFSIAEKNSYFDMNIVTQMKQRC 399  
Db 1092 HTNSTSEPKSH-NPPLLHCSAGVGTGFWILSEIMVACLSEHNEVLDIRVLDMLRQRM 1150  
QY 400 GMIQTEQYQCYEIVLEVLQ 421  
Db 1151 MLVQTLGQYFTVRVLIQFLKS 1172  
RESULT 10  
PTN4\_HUMAN STANDARD; PRT; 926 AA.  
ID PTN4\_HUMAN  
AC P29074;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Protein tyrosine phosphatase, non-receptor type 4 (EC 3.1.3.48)  
DE {protein-tyrosine phosphatase MEG1} (PTase-MEG1) (MEG).  
GN PTPN4.

Homo sapiens (Human).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 SEQUENCE FROM N.A.  
 MEDLINE=91288564; PubMed=1648233;  
 Gu M., York J.D., Marshawsky I., Majerus P.W.;  
 "Identification, cloning, and expression of a cytosolic megakaryocyte  
 protein-tyrosine-phosphatase with sequence homology to cytoskeletal  
 protein 4.1.";  
 Proc. Natl. Acad. Sci. U.S.A. 88:5867-5871(1991).  
 [2]  
 SEQUENCE FROM N.A.  
 TISSUE=Colon;  
 MEDLINE=22388257; PubMed=12477932;  
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 -!- FUNCTION: May act at junctions between the membrane and the  
 cytoskeleton.  
 -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 tyrosine + phosphate.  
 -!- SIMILARITY: Contains 1 FERM domain.  
 -!- SIMILARITY: Contains 1 PDZ/DHR domain.  
 -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
 Non-receptor class subfamily.  
 -----  
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 or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
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 EMBL; M68941; AAA36530.1; -.  
 EMBL; BC010674; AAH10674.1; -.  
 PIR; A41105; A41105.  
 HSP; P29350; IGWZ.  
 Genew; HGNC:9656; PRP4.  
 MIM; 176878; -.  
 GO; GO:0005737; Cytoplasm; TAS.  
 GO; GO:004726; F:non-membrane spanning protein tyrosine phosph. . .; TAS.  
 GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.  
 InterPro; IPR000299; Band\_4.1.  
 InterPro; IPR001478; PDZ.  
 InterPro; IPR000387; Tyr\_phosphatase.  
 InterPro; IPR000242; Tyr\_PP.  
 Pfam; PF00373; Band\_41; 1.  
 Pfam; PF00595; PDZ; 1.  
 Pfam; PF00102; Y\_phosphatase; 1.  
 PRINTS; PR00935; BAND41.  
 PRINTS; PR00700; PRTPHPTASE.  
 SMART; SM00295; B41; 1.  
 SMART; SM00228; PDZ; 1.

SMART; SM00194; PTPC; 1.  
 PROSITE; PS00660; FERM\_1; 1.  
 PROSITE; PS00661; FERM\_2; 1.  
 PROSITE; PS00557; FERM\_3; 1.  
 PROSITE; PS01066; PDZ; 1.  
 PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 PROSITE; PS00556; TYR\_PHOSPHATASE\_2; 1.  
 PROSITE; PS00555; TYR\_PHOSPHATASE\_PTP; 1.  
 Structural protein; Cytoskeleton; Hydrolase.  
 DOMAIN 29 312 FERM.  
 FT DOMAIN 517 589 PDZ.  
 FT DOMAIN 677 926 PROTEIN-TYROSINE PHOSPHATASE.  
 FT ACT\_SITE 852 852 PHOSPHOCYSTEINE INTERMEDIATE  
 (BY SIMILARITY).  
 FT SEQUENCE 926 AA; 105911 MW; 4DAC6A87A675CFB0 CRC64;  
 Query Match 21.4%; Score 478.5; DB 1; Length 926;  
 Best Local Similarity 27.9%; Pred. No. 1.8e-25;  
 Matches 127; Conservative 67; Mismatches 172; Indels 89; Gaps 9;  
 QY 24 NLNLRNSLPSSSSOKMTPTKPIFGNKNSENVKPSGHLSFSDKYELVYPEPLESDTDTVM 83  
 DB 490 HINETFDIPSSPEKFTPNGGPHENLVLRMKPDENGEGFENKGGYDKMPVIVSRVA- 548  
 QY 84 DVSDRLNRNMSMDSETAGSKTVSPVLSGSSRLSKDTSVSEKELTQLAQIRLPIFN 143  
 DB 549 -----PGTPADLCVPRNEGQVVLINGRDIAEHTHDQVV-----LPIK 587  
 QY 144 SSARSAMRDLNTLQKKEELDIIRFELE-----QMTLP 178  
 DB 588 ASCEHSGELMLLRPNVAVDVVEKLENEPQVPEKAPLDSVHDDHLSRSMQLA 647  
 QY 179 DFNSNGNL-----QNRDKRYRDLPYDSTRVPLGKKNKYNA 217  
 DB 648 EGLITGTVLTQDQLYRKKGWMTASCALPQNIKNRYDISPYDATRVILKGNEDYNA 707  
 QY 218 SVIR-----IVHREYFYIATQGLPETIEFWQVLENNCNVAMITREIECGVIK 270  
 DB 708 NYINMEIPSSIIHQ-----YIACQPLPHTCTDFWQMTWEGSSVMVNLTTQVERGRVK 762  
 QY 271 CYSYMPISLKEPLFEHFSVLETFVHTVYPTVTRVFQ---IVKSTGKSCQVHQLQTKW 327  
 DB 763 CHQYWP-----EPTGSSSYGCVVICHSEBGNATVIFRKMVLFNCKNESRPLTQIQYLA 818  
 QY 328 PDHGTPASADPFIKYRVYRKSHI--TGPLLHCSAGVGTGTFICVDVVFSALEKQYSP 385  
 DB 819 PDHGVDDSDFLDFVCHVRNKRAGKEEPVYVHCSAGIGTGVLTITXETAMCLIECNPV 878  
 QY 386 DTMNVTQMRKORCGMIOTKEQYQCYEIVLEVLQ 420  
 DB 879 YPLDIVTRDRQRMMIQTQSYRFVCEALKVYE 913  
 RESULT 11  
 PTP\_MOUSE  
 ID PTP\_MOUSE STANDARD; PRT; 1454 AA.  
 AC Q99M80; Q99M81; Q99M82; Q9J1Z1; Q9J1Z2; Q9J1Z3; Q9J1Z4; Q9J1Z5;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Receptor-type protein-tyrosine phosphatase T precursor (EC 3.1.3.48)  
 DE (R-FTP-T) (RPTP-rho) (mRPTPrho) (RPTPfam4).  
 GN PTPRT.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 5), AND ALTERNATIVE SPLICING.  
 RC STRAIN=C57BL/6J;  
 RA MEDLINE=22730707; PubMed=11423001;  
 RA Besco J.A., Frotschalm A., Popesco M.C., Burghes A.H.M., Rottler A.;  
 "Genomic organization and alternative splicing of the human and mouse

```

IT RPTPrho genes.";
IL BMC Genomics 2:1-1(2001).
IN [2]
IP ERATUM
XA MEDLINE=22730717; PubMed=11814386;
L Besco J.A., Frostholt A., Popesco M.C., Burghes A.H.M., Rotter A.;
L BMC Genomics 2:5-5(2001).
IN [3]
N N SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
P Buchli A.D., Zimmermann D.R., Pfister P., Vaughan L.;
T "RPTPrho": a fourth member of the MAM family of receptor protein
L tyrosine phosphatases expressed in adult brain.";
L Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
IN [4]
P SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
X MEDLINE=98146229; PubMed=9486824;
A McAndrew P.E., Frostholt A., Evans J.E., Zdilar D., Goldowitz D.,
A Chiu I.-M., Burghes A.H.M., Rotter A.;
T "Novel receptor protein tyrosine phosphatase (RPTPrho) and acidic
T fibroblast growth factor (FGF-1) transcripts delineate a rostrocaudal
T boundary in the granule cell layer of the murine cerebellar cortex.";
T J. Comp. Neurol. 391:444-455(1998).
L L -!- FUNCTION: May be involved in both signal transduction and cellular
C adhesion in the CNS. May have specific signaling roles in the
C tyrosine phosphorylation/dephosphorylation pathway in the anterior
C compartment of the adult cerebellar cortex.
C -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
C tyrosine + phosphate.
C -!- SUBCELLULAR LOCATION: Type I membrane protein.
C -!- ALTERNATIVE PRODUCTS:
C Event=Alternative splicing; Named isoforms=5;
C Name=1;
C IsoId=Q99M80-1; Sequence=Displayed;
C Name=2;
C IsoId=Q99M80-2; Sequence=VSP_007803, VSP_007806;
C Name=3; Synonyms=RPTPrho2;
C IsoId=Q99M80-3; Sequence=VSP_007803, VSP_007804;
C Name=4; Synonyms=RPTPrho1;
C IsoId=Q99M80-4; Sequence=VSP_007803;
C Name=5;
C IsoId=Q99M80-5; Sequence=VSP_007803, VSP_007805;
C -!- TISSUE SPECIFICITY: Expression is restricted to the CNS.
C Distributed throughout the brain and spinal cord.
C -!- DEVELOPMENTAL STAGE: Exceptionally high levels found in the cortex
C and olfactory bulbs during perinatal development and are down-
C regulated during postnatal week 2. Expression in the cerebellar
C cortex is restricted to the granule cell layer of lobules 1-6.
C Anterior and posterior compartments become discernible only during
C postnatal weeks 2 and 6.
C -!- SIMILARITY: Contains 1 MAM domain.
C -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
C -!- SIMILARITY: Contains 4 fibronectin type III domains.
C -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
C This SWISS-PROT entry is copyright. It is produced through a collaboration
C between the Swiss Institute of Bioinformatics and the EMBL outstation -
C the European Bioinformatics Institute. There are no restrictions on its
C use by non-profit institutions as long as its content is in no way
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C or send an email to license@isb-sib.ch).
C -----
C EMBL; AF152556; AAK34158.4; -.
C EMBL; AY026861; AAK18741.1; -.
C EMBL; AY026862; AAK18742.1; -.
C EMBL; AY026863; AAK18743.1; -.

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DR EMBL; AF244125; AAF44712.1; -.
DR EMBL; AF162856; AAF82400.2; -.
DR EMBL; AF162857; AAF82401.1; -.
DR HSP; P28827; IRPM.
DR MGD; MG1:1321152; Ptptr.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR000998; MAM domain.
DR InterPro; IPR003595; PTPC motif.
DR InterPro; IPR003387; TYR_PTPase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00623; MAM; 1.
DR Pfam; PF00102; Y_PTPase; 2.
DR PRINTS; PR00020; MAMDOMAIN.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00194; PTPC; 2.
DR SMART; SM00404; PTPC motif; 2.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00740; MAM 1; 1.
DR PROSITE; PS00660; MAM 2; 1.
DR PROSITE; PS00383; TYR_PTPase 1; 2.
DR PROSITE; PS00356; TYR_PTPase 2; 2.
DR PROSITE; PS00355; TYR_PTPase_FTP; 2.
DR Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
KW Immunoglobulin domain; Repeat; Alternative splicing.
FT SIGNAL 1 29
FT CHAIN 30 1454
FT RECEPTOR-TYPE PROTEIN-TYROSINE
FT PHOSPHATASE T.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT MAM.
FT IG-LIKE C2-TYPE.
FT FIBRONECTIN TYPE-III 1.
FT FIBRONECTIN TYPE-III 2.
FT FIBRONECTIN TYPE-III 3.
FT FIBRONECTIN TYPE-III 4.
FT PROTEIN-TYROSINE PHOSPHATASE 1.
FT PROTEIN-TYROSINE PHOSPHATASE 2.
FT PHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY).
FT PHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY).
FT POTENTIAL.
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT Missing (in isoform 2, isoform 3,
FT isoform 4 and isoform 5).
FT /FTId=VSP_007803. (in isoform 3).
FT R -> RNAYSYSYL (in isoform 5).
FT /FTId=VSP_007804.
FT R -> RNAYSYSYLSQR (in isoform 5).
FT /FTId=VSP_007805.
FT R -> RHPAHTVGTATLGRAASPGM (in isoform
FT 2).
FT /FTId=VSP_007806.
FT MISSING (IN REF. 1).
FT R -> P (IN REF. 1).
FT GGCS -> RGVF (IN REF. 1).
FT A -> T (IN REF. 4; AAF82401).
FT A -> S (IN REF. 4; AAF82401).
FT I -> V (IN REF. 4; AAF82401).

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CONFLICT 602 602 T -> S (IN REF. 4; AAF82401).  
 CONFLICT 822 822 A -> T (IN REF. 4; AAF82401).  
 CONFLICT 825 825 G -> S (IN REF. 4; AAF82401).  
 CONFLICT 844 845 TD -> N (IN REF. 4; AAF82401).  
 CONFLICT 1016 1016 D -> A (IN REF. 4; AAF82401).  
 CONFLICT 1049 1049 Y -> H (IN REF. 1).  
 CONFLICT 1050 1050 L -> V (IN REF. 4; AAF82401).  
 CONFLICT 1076 1076 H -> V (IN REF. 4; AAF82401).  
 CONFLICT 1103 1103 R -> K (IN REF. 1).  
 CONFLICT 1259 1259 F -> L (IN REF. 4; AAF82401).  
 CONFLICT 1266 1266 L -> I (IN REF. 4; AAF82401).  
 CONFLICT 1269 1269 T -> S (IN REF. 4; AAF82401).  
 SEQUENCE 1454 AA; 163012 MM; C60464F7B423F8A8 CRC64;  
 Query Match 21.3%; Score 477.5; DB 1; Length 1454;  
 Best Local Similarity 28.5%; Pred. No. 3.7e-25;  
 Matches 137; Conservative 65; Mismatches 160; Indels 119; Gaps 16;  
 15 NDEEGNSGMLNRLNSLSSSQMTPPTPI-----FGNKNSENKVPKSHLSFSDKYELVY 70  
 716 NGETKINCVRATKGA-PMGSAQVTPGTCLLTASTQNTVEP----- 760  
 71 PPLESDTDETV-----WDVSDRLNRNWSMDSETAGSKTVSP 110  
 761 ----EKQDNTVWAGVIAGLMLFIILLGVMLTKRKLAKKETQS---GAQREMG 813  
 111 VLS-----GSRLSKQTE--TSVSEKELTQLA----- 135  
 814 VASTDKPTAKLTNRNDEGFSSSQDVNGFTDGRGSLQPTLIQTHPYRTCDPVMSY 873  
 136 ---QIRPLIFNSSARSAMEDCLNTLOK-----KEELDIREFLELQMTLPDPFNS 183  
 874 PDQFQPAI-----RVADLLQHTQMRGGYGFKEEYALPEGQTASWDTKED--- 923  
 184 GNTLQNRDKRYRDLPLDYSTRVPL-----GKNQDYINASYIRIWNHEERYFYIATQCP 238  
 924 ---ENRNKRYGNIISYDHSVRLLVLDGPHSDYINANYID--GYHRPHVIATQGM 977  
 239 PETIDFQOMVLNNCNVIAMTIREGCVKCYSWPISLKBPLEFHEFHSVFLEPHVT 298  
 978 QETVDFRMIQWENSASIVMTNLVEGRVKRYNPDPTFVYGDIK--VTLIETPLA 1035  
 299 QYTVRVQIVKSGKQCVKHLQFTKWDPHGTPASADPFIKVRYVR--KSHITGPLL 356  
 1036 EV-VIRTTVQKKGHEIRLHFHTSWPHGUPCYATGLLGFVRQKFLNPEAGPIV 1094  
 357 VHCASGAGRTGVFCVDFVFAIRNYSFDIMNIVTQMRQRCGMIQKEQYQFCYEIVL 416  
 1095 VHCASAGAGRTGCFIAIDTMDLWDAENEGVVDIFNCVRELRAQVNLQTERQYVFEVDAIL 1154  
 417 E 417  
 1155 E 1155

## RESULT 12

PTPT HUMAN STANDARD; PRT: 1463 AA.  
 O14522; O43655; O75664; Q9BR24; Q9BR28; Q9H0Y8; Q9NTL1; Q9NU72;  
 Q9UBD2; Q9JUL7;  
 10-OCT-2003 (Rel. 42, Created)  
 10-OCT-2003 (Rel. 42, Last sequence update)  
 10-OCT-2003 (Rel. 42, Last annotation update)  
 Receptor-type protein-tyrosine phosphatase T precursor (EC 3.1.3.48)  
 (R-PTP-T) (RPTP-tho).  
 PTPT OR KIAA0283.  
 Homo sapiens (Human).  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  
 [1]  
 NCBI TaxID=9606;  
 SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.  
 MEDLINE=98267260; PubMed=9602027;

RA McAndrew P.E., Frostholt A., White R.A., Rotter A., Burghes A.H.M.;  
 RT "Identification and characterization of RPTP rho, a novel RPTP  
 RT mu/kappa-like receptor protein tyrosine phosphatase whose expression  
 RT is restricted to the central nervous system.";  
 RL Brain Res. Mol. Brain Res. 56:9-21(1998).  
 RN [2]  
 RN SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Brain;  
 RX MEDLINE=97323006; PubMed=9179496;  
 RA Ohara O., Nagase T., Ishikawa K.-I., Nakajima D., Ohira M.,  
 RA Seki N., Nomura N.;  
 RT "Construction and characterization of human brain cDNA libraries  
 RT suitable for analysis of cDNA clones encoding relatively large  
 RT proteins.";  
 RL DNA Res. 4:53-59(1997).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
 RA Bailey J., Barlow K.P., Bates K.N., Beare D.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Copley V.B., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhali P.D., Dunn M.,  
 RA Gillington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Levaeslatho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.P., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb S.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
 RA Skuce C.D., Smith M.B., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A.L., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 RN [4]  
 RN ALTERNATIVE SPLICING.  
 RX MEDLINE=22730707; PubMed=11423001;  
 RA Besco J.A., Frostholt A., Popesco M.C., Burghes A.H.M., Rotter A.;  
 RT "Genomic organization and alternative splicing of the human and mouse  
 RT RPTPrho genes.";  
 RL BMC Genomics 2:1-1(2001).  
 RN [5]  
 RN ERRATUM.  
 RX MEDLINE=22730717; PubMed=11814386;  
 RA Besco J.A., Frostholt A., Popesco M.C., Burghes A.H.M., Rotter A.;  
 RL BMC Genomics 2:5-5(2001).  
 CC -!- FUNCTION: May be involved in both signal transduction and cellular  
 CC adhesion in the CNS.  
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=O14522-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=O14522-2; Sequence=VSP\_007802;  
 CC -!- TISSUE SPECIFICITY: Expression is restricted to the CNS.  
 CC -!- SIMILARITY: Contains 1 MAM domain.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC -!- SIMILARITY: Contains 4 fibronectin type III domains.  
 CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.

-----  
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 R EMBL; AFO43644; AAD09421.2; -  
 R EMBL; AFO06621; BAA22952.2; ALT\_INIT.  
 R EMBL; AL021395; CAC24740.2; -  
 R EMBL; AL022239; CAC26785.1; -  
 R EMBL; AL024473; CAA19666.1; -  
 R EMBL; AL031856; CAA17521.1; -  
 R EMBL; AL049812; CAB92429.1; -  
 R EMBL; AL121763; CAC21701.1; -  
 R EMBL; AL136461; CAB91828.1; -  
 R EMBL; Z93942; CAC26841.1; -  
 R HSP; P28827; IRPX.  
 R Genes; HGNC:9682; PTPRT.  
 R GO; GO:0005887; C: integral to plasma membrane; TAS.  
 R GO; GO:0005901; P: transmembrane receptor protein tyrosine pho. . .; TAS.  
 R GO; GO:0006470; P: protein amino acid dephosphorylation; TAS.  
 R GO; GO:0007169; P: transmembrane receptor protein tyrosine kin. . .; TAS.  
 R InterPro; IPR003961; FN III.  
 R InterPro; IPR007110; IG-like.  
 R InterPro; IPR000998; NAM domain.  
 R InterPro; IPR003595; PTPC motif.  
 R InterPro; IPR000387; Tyr Phosphatase.  
 R InterPro; IPR000242; Tyr\_PP.  
 R Pfam; PF00041; fn3; 3.  
 R Pfam; PF00629; NAM; 1.  
 R Pfam; PF00102; Y Phosphatase; 2.  
 R PRINTS; PR00020; NAMEDOMAIN.  
 R PRINTS; PR00700; PRTYPHPTASE.  
 R SMART; SM00060; FN3; 3.  
 R SMART; SM00137; NAM; 1.  
 R SMART; SM00194; PTPC; 2.  
 R SMART; SM00404; PTPC motif; 2.  
 R PROSITE; PS50835; IG LIKE; 1.  
 R PROSITE; PS00740; NAM; 1; 1.  
 R PROSITE; PS00660; NAM; 2; 1.  
 R PROSITE; PS00383; TYR PHOSPHATASE 1; 2.  
 R PROSITE; PS00383; TYR PHOSPHATASE 2; 2.  
 R PROSITE; PS50056; TYR PHOSPHATASE PTP; 2.  
 R PROSITE; PS50055; TYR PHOSPHATASE; 2.  
 R Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;  
 M Immunoglobulin domain; Repeat; Alternative splicing.  
 W SIGNAL 1 25 POTENTIAL.  
 T CHAIN 26 1463 RECEPTOR-TYPE PROTEIN-TYROSINE  
 T DOMAIN 26 766 PHOSPHATASE T.  
 T TRANSMEM 767 787 EXTRACELLULAR (POTENTIAL).  
 T DOMAIN 788 1463 POTENTIAL.  
 T DOMAIN 30 191 CYTOPLASMIC (POTENTIAL).  
 T DOMAIN 193 284 MAM.  
 T DOMAIN 289 374 IG-LIKE C2-TYPE.  
 T DOMAIN 386 480 FIBRONECTIN TYPE-III 1.  
 T DOMAIN 481 584 FIBRONECTIN TYPE-III 2.  
 T DOMAIN 589 726 FIBRONECTIN TYPE-III 3.  
 T DOMAIN 911 1165 FIBRONECTIN TYPE-III 4.  
 T DOMAIN 1197 1459 PROTEIN-TYROSINE PHOSPHATASE 1.  
 T ACT\_SITE 1106 1106 PROTEIN-TYROSINE PHOSPHATASE 2.  
 T PHOSPHOCYSTEINE INTERMEDIATE (BY  
 T SIMILARITY).  
 T PHOSPHOCYSTEINE INTERMEDIATE (BY  
 T SIMILARITY).  
 T ACT\_SITE 1400 1400 POTENTIAL.  
 T DISULFID 213 267 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 T CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 T CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 T CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 T CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 T CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 T CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 510 510 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 547 547 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 654 654 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 684 684 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 726 744 Missing (in isoform 2).  
 FT CONFLICT 29 29 /FTID=VSP\_007802.  
 FT CONFLICT 60 60 P -> A (IN REF. 3).  
 FT CONFLICT 375 375 T -> W (IN REF. 1).  
 FT CONFLICT 801 803 A -> P (IN REF. 1).  
 FT CONFLICT 889 889 MISSING (IN REF. 1).  
 FT CONFLICT 889 889 L -> P (IN REF. 1).  
 SQ SEQUENCE 1463 AA; 164275 MW; BE4BA8B3E8A4017 CRC64;  
 Query Match 21.3%; Score 477; DB 1; Length 1463;  
 Best Local Similarity 28.5%; Pred. No. 4.1e-25;  
 Matches 137; Conservative 63; Mismatches 158; Indels 122; Gaps 16;  
 Qy 25 LALRLSLPSSSKMTPTKPIF-----GNKMSENVKPSHLSFSDKYELVYEPLESDTD 79  
 Db 720 VLATKAPMGSAGVTPGTCLITTCASTQNSNTVEP-----EKQVD 761  
 Qy 80 ETY-----WDVSDRLNRNWSMDSETAGPSK 106  
 Db 762 NTKMAGVIAGLLMFIILLGVMLTKRRNAYSYYLSQKLAQKQKQTS---GAQR 818  
 Qy 107 TVSPVLS-----GSSFLSKDTE--TSVSEKELTO---LAQIRPL----- 140  
 Db 819 EMGFVASADKPTTKLSASNDGFSSSQDVNGFTDGGSGELQFTLIQTHPTCTDPV 878  
 Qy 141 -----IFNSSARSAMRDCLNTLQK-----KEELDIIRFLELEQMTLPDPFNSG 184  
 Db 879 ENSYPRDQFQLAIRVA--DLLQHITCMKRGQGYGPKVEEALPEGQTASWDTKED--- 932  
 Qy 185 NTLQNRDKRYRDILPYDSTRVPL-----GKNKYDINASYIRIVNHEEYFVIATQGLP 239  
 Db 933 ---ENRKNRYGNIISYDHSRVRLVLDGPHSDVINANYID--GYHPRHYIATQGMQ 987  
 Qy 240 ETIEDFWQVLNENNCNVIAMITREIECGVVKCYSPISLKEPLEFEHFSVFLEFHYTQ 299  
 Db 988 ETVKDFRMIMQENSASIVMTNLVEGVRKCVRWPDTEVYGDIK--VTLIETEPALAE 1045  
 Qy 300 YFTVRVFOIVKSTGKSCQVKEHQTKPDHGTASADFFIKYVYVR--KSHITGPIIV 357  
 Db 1046 Y-VIRFTYQKGYHIRELRFLHFTSPDHPGVCYATGLGLGFVRKVLNPPPEAGPIV 1104  
 Qy 358 HCSAGVGRGVFCVDVVPFSAJEKNYSFDIMNIVQMQRKQRCMIQKQYQFCYEVILE 417  
 Db 1105 HCSAGVGRGVFCIADTMDLMAENSGVDIFNCVRELRARQVNLVQTEEQYVVFVDAILE 1164  
 RESULT 13  
 PTPB HUMAN  
 ID\_PTPB HUMAN STANDARD; PRT; 1997 AA.  
 AC P23457;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase beta precursor (EC 3.1.3.48) (R-PTP-beta).  
 DE beta).  
 GN PTPRB OR PTPB.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=91006018; PubMed=2170109;  
 RA Krueger N.X., Streuli M., Saito H.;  
 RT "Structural diversity and evolution of human receptor-like protein  
 RT tyrosine phosphatases.";  
 RL EMBO J. 9:3241-3252(1990).









GenCore version 5.1.6  
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M protein - protein search, using sw model

un on: June 16, 2004, 13:17:25 ; Search time 46 Seconds  
(without alignments)  
2921.973 Million cell updates/sec

title: US-09-095-478A-5

effect score: 2241

sequence: 1 MSPKRVKTKGRDNDEBG.....QYQFCYIVLEVQLNLLALY 426

coring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

searched: 1017041 seqs, 31518202 residues

total number of hits satisfying chosen parameters: 1017041

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

- SPTREMBL.25:\*
- 1: sp.archaea:\*
  - 2: sp.bacteria:\*
  - 3: sp.fungi:\*
  - 4: sp.human:\*
  - 5: sp.invertebrate:\*
  - 6: sp.mammal:\*
  - 7: sp.mhc:\*
  - 8: sp.organelle:\*
  - 9: sp.phage:\*
  - 10: sp.plant:\*
  - 11: sp.rodent:\*
  - 12: sp.virus:\*
  - 13: sp.vertebrate:\*
  - 14: sp.unclassified:\*
  - 15: sp.yvirus:\*
  - 16: sp.bacteriap:\*
  - 17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

result No.	Score	Match	Length	DB	ID	Description
1	2241	100.0	426	11	O55082	O55082 mus musculus
2	1310	58.5	398	4	Q9Y405	Q9Y405 homo sapien
3	660	29.5	2460	11	O44512	O44512 mus musculus
4	655.5	29.3	2484	6	Q28006	Q28006 bos taurus
5	500	22.3	292	4	Q8N4S3	Q8N4S3 homo sapien
6	497.5	22.2	2051	5	O44328	O44328 hirudo medi
7	496.5	22.2	615	13	Q9IAI8	Q9IAI8 xenopus lae
8	495.5	22.1	926	11	Q9WU22	Q9WU22 mus musculus
9	494	22.0	849	11	O3TLJ8	O3TLJ8 mus musculus
10	493.5	22.0	468	13	Q3IEA0	Q3IEA0 potamoxygo
11	493.5	22.0	857	13	Q90Y04	Q90Y04 brachydanio
12	491.5	21.9	468	13	Q9IBA2	Q9IBA2 potamoxygo
13	490.5	21.9	1502	4	Q9UM81	Q9UM81 homo sapien
14	490	21.9	832	13	Q90947	Q90947 gallus gall
15	489.5	21.8	749	11	Q8R169	Q8R169 mus musculus
16	489.5	21.8	1254	11	Q8VBV0	Q8VBV0 mus musculus

17	488.5	21.8	758	11	Q7TMG1	Q7TMG1 mus musculus
18	486	21.7	468	13	Q9NL06	Q9NL06 eptatretus
19	484	21.6	1222	13	Q8MY44	Q8MY44 eptatretus
20	484	21.6	1896	13	Q9IAJ1	Q9IAJ1 xenopus lae
21	483	21.6	1100	13	Q8MY45	Q8MY45 eptatretus
22	483	21.6	1187	13	Q8MY42	Q8MY42 eptatretus
23	483	21.6	1202	13	Q8MY43	Q8MY43 eptatretus
24	483	21.6	1499	13	Q90815	Q90815 gallus gall
25	480	21.4	694	13	Q72YN2	Q72YN2 xenopus lae
26	479.5	21.4	459	13	Q9NL08	Q9NL08 eptatretus
27	479	21.4	597	13	Q91871	Q91871 xenopus lae
28	478.5	21.4	469	5	Q9NLI1	Q9NLI1 branchiosteo
29	478.5	21.4	907	13	Q8MY41	Q8MY41 eptatretus
30	478	21.3	1238	11	Q8K3Q2	Q8K3Q2 mus musculus
31	477.5	21.3	1501	11	Q7TT17	Q7TT17 mus musculus
32	476.5	21.3	1501	11	Q9QW00	Q9QW00 rattus sp.
33	476.5	21.3	1863	11	O64605	O64605 rattus norv
34	476	21.2	1216	11	Q82884	Q82884 rattus norv
35	476	21.2	1406	13	Q9W6V5	Q9W6V5 gallus gall
36	475.5	21.2	1998	11	Q8CIW2	Q8CIW2 mus musculus
37	475	21.2	361	11	Q61373	Q61373 mus musculus
38	475	21.2	694	13	Q91870	Q91870 xenopus lae
39	475	21.2	1024	4	Q8WX29	Q8WX29 homo sapien
40	474.5	21.2	1156	5	Q21214	Q21214 caenorhabdi
41	474.5	21.2	1304	11	Q84699	Q84699 mus musculus
42	473.5	21.1	498	5	Q8IRM6	Q8IRM6 drosophila
43	473.5	21.1	578	5	Q9W324	Q9W324 drosophila
44	473.5	21.1	797	5	Q8IRM7	Q8IRM7 drosophila
45	473.5	21.1	827	5	Q9W323	Q9W323 drosophila

#### ALIGNMENTS

#### RESULT 1

O55082 ID O55082 PRELIMINARY; PRT; 426 AA.  
AC O55082;  
DT 01-JUN-1998 (TREMBlrel. 06, Created)  
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Protein-tyrosine-phosphatase (EC 3.1.3.48).  
GN PTPN20.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RX MEDLINE=98070510; PubMed=9407093;  
RA Ohnogi M., Kuramochi S., Matsuda S., Yamamoto T.;  
RT "Molecular cloning and characterization of a novel cytoplasmic  
RT protein-tyrosine phosphatase that is specifically expressed in  
RT spermatocytes.";  
RL J. Biol. Chem. 272:33092-33099(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RL ENBL; D64141; BAA23761.1; --  
DR ENBL; AK029493; BAC28476.1; --  
DR HSSP; Q6e124; 2SHP.  
DR MGD; MGI:1196295; Ptpn20.  
DR GO; GO:0016787; F:phosphatase activity; IEA.  
DR GO; GO:004727; F:phosphorylated protein tyrosine phosphatase act. .; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000397; TYR\_phosphatase.

December

R InterPro; IPR000242; Tyr\_PP.  
R Pfam; PF00102; Y\_phosphatase; 1.  
R PRINTS; PR00700; PRTYPPHPTASE.  
R SMART; SM00194; PTPC; 1.  
R PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
R PROSITE; PS00383; TYR\_PHOSPHATASE\_2; 1.  
R PROSITE; PS00056; TYR\_PHOSPHATASE\_1; 1.  
R PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
R PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
W Hypothetical protein; Hydrolase.  
Q SEQUENCE 426 AA; 49118 MW; 2B35FB13379502F4 CRC64;

Query Match 100.0%; Score 2241; DB 11; Length 426;  
Best Local Similarity 100.0%; Pred. No. 5.4e-167;  
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MSSPRKVRGKTGRNDDEEGNSGNLNRSLPSSSQKMTPTKPIFGKXNSENKPKSHL 60  
b 1 MSSPRKVRGKTGRNDDEEGNSGNLNRSLPSSSQKMTPTKPIFGKXNSENKPKSHL 60  
Y 61 SPDKYELVYPELESDDTETVWDVSDRLNRNMSDSETAGSKTVSPVLSSSRLSK 120  
b 61 SPDKYELVYPELESDDTETVWDVSDRLNRNMSDSETAGSKTVSPVLSSSRLSK 120  
Y 121 DTSVSEKELTQIAQIRPLIFNSSARSAMDCLNTLQKKEBDDIIRBFELEQMTLPDD 180  
b 121 DTSVSEKELTQIAQIRPLIFNSSARSAMDCLNTLQKKEBDDIIRBFELEQMTLPDD 180  
Y 181 FNSGNLQNRDKNRYDILPYDSTRVPLGKNDYINASYIRVWHEEYFYIATQGPLPE 240  
b 181 FNSGNLQNRDKNRYDILPYDSTRVPLGKNDYINASYIRVWHEEYFYIATQGPLPE 240  
Y 241 TIEDFWQVLENNCNVIAITREIECGVIKCYSYWPISLKEPLEFEHPSVLETFHVTQY 300  
b 241 TIEDFWQVLENNCNVIAITREIECGVIKCYSYWPISLKEPLEFEHPSVLETFHVTQY 300  
Y 301 FTVRVQIVKSKGQCVKHQFTKWPDKGTASADPFIKTVRVVRSKSHITGPLLHVC 360  
b 301 FTVRVQIVKSKGQCVKHQFTKWPDKGTASADPFIKTVRVVRSKSHITGPLLHVC 360  
Y 361 AGVGRGVFICVDVDFSAIEKNVSPDMMIVTOMKRGCMQTKQYQFCYVIVLEVLQ 420  
b 361 AGVGRGVFICVDVDFSAIEKNVSPDMMIVTOMKRGCMQTKQYQFCYVIVLEVLQ 420  
Y 421 NLALY 426  
b 421 NLALY 426

RESULT 2  
9Y406 PRELIMINARY; PRT; 398 AA.  
C Q9Y406  
T 01-NOV-1999 (TrEMBLrel. 12, Created)  
T 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
T 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
E Hypothetical protein (Fragment).  
N DKPZ566K0524.  
S Homo sapiens (Human).  
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
X NCBI\_TaxID=9606;  
N [1]  
N SEQUENCE FROM N.A.  
C TISSUE=Kidney;  
A Ausorge W., Winkner U., Mewes H.W., Gassenhuber J., Wiemann S.;  
L Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
R EMBL; AL050040; CAB43248.1; --  
R PIR; T08716; T08716.  
R HSP; Q06124; 2SHP.  
R GO; GO:0016787; F:hydrolase activity; IEA.  
R GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
R GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
R InterPro; IPR000387; TYR\_phosphatase.  
R InterPro; IPR000242; Tyr\_PP.

DR Pfam; PF00102; Y\_phosphatase; 1.  
DR PRINTS; PR00700; PRTYPPHPTASE.  
DR SMART; SM00194; PTPC; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
KW Hypothetical protein; Hydrolase.  
FT NON TER 1  
SQ SEQUENCE 398 AA; 45690 MW; 857AAD03747870A2 CRC64;

Query Match 58.5%; Score 1310; DB 4; Length 398;  
Best Local Similarity 65.4%; Pred. No. 3.3e-94;  
Matches 253; Conservative 48; Mismatches 78; Indels 8; Gaps 2;

QY 40 PTKPIFGKXNSENKPKSHLSFSDKYELVYPELESDDTETVWDVSDRLNRNMSD 99  
b 18 PQAQVFNKVNSEKVKLSLRNPFHNDYEDVPEPESGSDPSMWTARGPFRDRSSDE 77  
QY 100 ETAGPSKTVSPVLSSSRLSKDTETSVSEKELTQIAQIRPLIFNSSARSAMDCLNTLQK 159  
b 78 EAAGPSQALSPLLS-----DTRKIVSEGEUDQQAIRPLIFNFHBOIALKDKLLEE 130  
QY 160 K-BELDIIREFLEQMTLPDDFNSGNLQNRDKNRYDILPYDSTRVPLGKNDYINAS 218  
b 131 KTAAYDIMQBFMALEKLPGEFYSGNQPSNRKRYRDIILPYDSTRVPLGKNDYINAS 190  
QY 219 YIRVWHEEYFYIATQGPLPETIEDFWQVLENNCNVIAITREIECGVIKCYSYWPIS 278  
b 191 YIRVWHEEYFYIATQGPLPETIEDFWQVLENNCNVIAITREIECGVIKCYSYWPIS 250  
QY 279 LKEPLFEHPSVLETFHVTQYFTRVQIVKSKGQCVKHQFTKWPDKGTASADP 338  
b 251 LKPLSLKHFRVLENNYQLQYFIIRMFQVVEKSTGTSVSKQLQFTKWPDKGTASADS 310  
QY 339 FIKTVRVKSKSHITGPLLHVCAGVGRGVFICVDVDFSAIEKNVSPDMMIVTOMK 398  
b 311 FIKTVRVKSKSHITGPLLHVCAGVGRGVFICVDVDFSAIEKNVSPDMMIVTOMK 370  
QY 399 CGMIQTKQYQFCYVIVLEVLQMLAL 425  
b 371 SGVQTKQYQFCYVIVLEVLQMLAL 397

RESULT 3  
Q64512 PRELIMINARY; PRT; 2460 AA.  
AC Q64512 Q62135; Q61494; Q64499.  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Protein-tyrosine phosphatase, NONRECEPTOR-type, 13 (EC 3.1.3.48)  
DE (Protein-tyrosine phosphatase RIP) (Phosphoprotein phosphatase)  
DE (Protein-tyrosine-phosphatase) (Phosphotyrosine phosphatase) (PTPASE)  
DE (PTP36)  
GN PTPN13 OR PTP14.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=SKIN;  
RX MEDLINE=96340953; PubMed=8749712;  
RA Hendriks W., Schepens J., Baechner D., Rijss J., Zeeuwen P.,  
RA Zechner U., Hameister H., Wieringa B.;  
RT "Molecular cloning of a mouse epithelial protein-tyrosine phosphatase  
with similarities to submembranous proteins.";  
RL J. Cell. Biochem. 59:418-430(1995).  
RN [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=DEA/2;  
RX MEDLINE=95145716; PubMed=7843407;  
RA Chida D., Kume T., Mukoyama Y., Tabata S., Nomura N., Thomas M.,

REPEAT	1490	1577	DHR/GLGF REPEAT 3.
REPEAT	1763	1843	DHR/GLGF REPEAT 4.

DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)

0-10 100

BA14.  
Bos taurus (Bovine).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
NCBI\_TaxID=9913;  
[1]  
SEQUENCE FROM N.A.  
Vega Q.C., Walton K.M., Dixon J.E.;  
"Tyrosine phosphatases and the Cytoskeleton";  
Submitted (F88-1995) to the EMBL/GenBank/DBJ databases.  
EMBL; U20807; AAA73516.1;  
GO; GO:0005856; C:cytoskeleton; IEA.  
GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
GO; GO:0007242; P:intracellular signaling cascade; IEA.  
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
InterPro; IPR000299; Band 4.1.  
InterPro; IPR001478; PDZ.  
InterPro; IPR000387; Tyr\_phosphatase.  
InterPro; IPR000242; Tyr\_Pp.  
Pfam; PF00373; Band 41; 1.  
Pfam; PF00595; PDZ; 5.  
Pfam; PF00102; Y\_phosphatase; 1.  
PRINTS; PR00935; BAND4.  
PRINTS; PR00700; PTYPHPTASE.  
SMART; SM00295; B41; 1.  
SMART; SM00228; PDZ; 5.  
SMART; SM00194; PTPC; 1.  
PROSITE; PS00660; FERM\_1; FALSE\_NEG.  
PROSITE; PS00661; FERM\_2; FALSE\_NEG.  
PROSITE; PS00057; FERM\_3; 1.  
PROSITE; PS0106; PDZ; 5.  
PROSITE; PS00383; TYR\_PHOSPHATASE\_1; FALSE\_NEG.  
PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
SEQUENCE 2484 AA; 276382 MW; 45A92F0D4F1ED13D CRC64;  
Query Match 29.3%; Score 655.5; DB 6; Length 2484;  
Best Local Similarity 30.3%; Pred. No. 6.4e-42;  
Matches 151; Conservative 75; Mismatches 148; Indels 125; Gaps 8;  
32 PSSSQMTPKPIFGNKNNSNPKSPSHLSPSDKYELVPE-----72  
1993 PCGKPSLTPNNSF--SKVNGEEI-----IEILYPEGKSTYQMKESANLILYKE 2039  
73 -----PLESDTDETVMDVSDSLRN-----92  
2040 SDGQEDENYDDQAEVIOQLDYYDBEAQNLNQNNVAGDACVPGALKANEKLSERAO 2099  
93 -----RWNSMDSSETAGPSKTVSPVLGSSRLSKOTETS-----125  
2100 DTYCDGSLPDEPTSTWNGCEBCEKSKESLSIQKSEKKTEDDEITWGSDELPIET 2159  
126 -----VSEKELTOLAQIRPLIFNSSASAMEDCLNTLQ-----KKEELDII 166  
2160 TDHDSNKEHPLTNEELTPIIKVLPSPGKYTGAKLSVIRMLRGLLDGIGSKELDNL 2219  
167 REFLEQLMTLPDDFNSGNTLNQNRDILPYDSTRVPLGKNKDYINASYIRIVNHE 226  
2220 QELKELDQCLL-----GQTKENRRKNRYKNILPYDATRVPLGDEGGYINASFIKIPVGR 2273  
227 ERYFYATQGLPETHIEDFWQVLENNCNVIAMITREICGVIKCYSWPISLKEPLEF 285  
2274 EEFVYIACQGLPTFTVGFQWQVMEQNSSVTAMTQVEGEKIKCQRYWPNVLGKSTWS 2333  
286 EHFVSFLETFHTVQYFTVRVFOIVKSKGKQCKVKHLOFTKPDHGTSPASADPFKIVRY 345  
2334 NRIELALVRVQQLKGFVVRAMTLEDIQTEGVHRVSHLNFTAWPDHPTSPQDDLLTFISY 2393  
346 VRKSHITGPLLVHCSAGVGRGVFTICVDVVFSAIEKNYSFDIMNIVTMKQKQRCGMLOTK 405  
2394 MRVFRSGPIITHCSAGIGRGTLLCIDWNVLGLISQDLFEIDISLVRMCLQRHGMVQTE 2453

QY 406 EQYQCYEIVLEVLQNLIA 424  
Db 2454 DQYIFCYQVILYVULRLOA 2472  
RESULT 5  
Q8N4S3 PRELIMINARY; PRT; 292 AA.  
AC Q8N4S3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Renal adenocarcinoma;  
RA Strausberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC033716; AAR33716.1; -.  
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.  
DR GO; GO:0005488; F:binding; IEA.  
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR001993; Mitoch\_carrier.  
DR InterPro; IPR003595; PTPC motif.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR000242; Tyr\_Pp.  
DR Pfam; PF00102; Y\_phosphatase; 1.  
DR PRINTS; PR00700; PTYPHPTASE.  
DR SMART; SM00194; PTPC; 1.  
DR SMART; SM00404; PTPC\_motif; 1.  
DR PROSITE; PS00215; MITOCH\_CARRIER; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 292 AA; 33121 MW; 54B838BDD41D1BD7 CRC64;  
Query Match 22.3%; Score 500; DB 4; Length 292;  
Best Local Similarity 42.0%; Pred. No. 5.1e-31;  
Matches 102; Conservative 38; Mismatches 85; Indels 18; Gaps 5;  
QY 188 QNRDKRYRDLPYDSTRVPLGKNKDYINASYI-----RIVNHEEYFYIATQGLPE 240  
Db 48 QNLDKRYRDLPYDTRVLLQGNEDYINASYVNNETPAANLVNK-----YIATQGLPH 102  
QY 241 TIEDFWQVLENNCNVIAMITREICGVIKCYSWPISLKEPLEF--FSVLETFHVT 298  
Db 103 TCAQFWQVWQKLSLVMLTTLTGRGRTKCHQWP--DPPVMMHGGPHIQCSBDCT 159  
QY 299 QYFTVRVFOIVKSKGKQCKVKHLOFTKPDHGTSPASADPFKIVRYVRKSHI-TGPELLV 357  
Db 160 IAYVSRREMLVNTQTGEHTVTHLQYVAFPDHGVDPDSDSDFLEFWYVYRSLRVDSEPLV 219  
QY 358 HCSAGVGRGVFTICVDVVFSAIEKNYSFDIMNIVTMKQKQRCGMLOTKQYFCYIVLE 417  
Db 220 HCSAGIGRGTVLMETAMCLTERNLPIYPLDIVRKMRDQERAMNVQTSQYKFCVAILR 279  
QY 418 VILQ 420  
Db 280 VYE 282  
RESULT 6  
Q44328 PRELIMINARY; PRT; 2051 AA.  
ID O44328  
AC O44328;

01-JUN-1998 (TremBLrel. 06, Created)  
01-JUN-1998 (TremBLrel. 06, Last sequence update)  
01-OCT-2003 (TremBLrel. 25, Last annotation update)  
Receptor tyrosine phosphatase.  
HMLAR2.  
Hirudo medicinalis (Medicinal leech).  
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
Arychobdellida; Hirudiniformes; Hirudinidae; Hirudo.  
NCBI\_TaxID=6421;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=98195364; PubMed=9526016;  
Gershon T.R., Baker M.W., Nitsbach M., Wu P., Macagno E.R.;  
"Two receptor tyrosine phosphatases of the LAR family are expressed in  
the developing leech by specific central neurons as well as select  
peripheral neurons, muscles, and other cells.";  
J. Neurosci. 18:2991-3002(1998).  
EMBL; AF017083; AAB91460.1; --  
PIR; T30938; T30938.  
HSP; F28827; IRPM.  
GO; GO:0016787; F:hydrolase activity; IEA.  
GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
InterPro; IPR003962; FNIII subd.  
InterPro; IPR003961; FN III  
InterPro; IPR008957; FN-III-like.  
InterPro; IPR007110; IG-like.  
InterPro; IPR003598; IG\_c2.  
InterPro; IPR003387; TYR\_phosphatase.  
InterPro; IPR000242; Tyr\_PP.  
Pfam; PF00043; fn3; 8.  
Pfam; PF00047; ig; 3.  
Pfam; PF00102; Y\_phosphatase; 2.  
PRINTS; PR00014; FNTPHPTASE.  
PRINTS; PR00700; PRTYPHPTASE.  
SMART; SM00060; FN3; 7.  
SMART; SM00408; IGc2; 3.  
SMART; SM00194; PTPC; 2.  
PROSITE; PS00835; IG LIKE; 3.  
PROSITE; PS00383; TYR\_PHOSPHATASE 1; 2.  
PROSITE; PS00056; TYR\_PHOSPHATASE 2; 2.  
PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
Hydrolase; Immunoglobulin domain; Repeat.  
SEQUENCE 2051 AA; 229604 MW; D60F8A032P659B00 CRC64;  
Query Match 22.2%; Score 497.5; DB 5; Length 2051;  
Best Local Similarity 31.8%; Pred. No. 1.1e-29;  
Matches 125; Conservative 69; Mismatches 134; Indels 65; Caps 12;  
37 KMTPTKPIFGNRMSENKPSHLSFSDKYLVPPEPESDSDTDTVMDVSDRLNRWNS 96  
1706 KHTGSDVLYGH-VTCLRAQRNMYVQTEQVIFHAILEAVTSNT-EVPARNL----- 1757  
97 MDSETAGSKTVSPVLSGSSRLSDTSTVSEKELTOLAQIRLIPNSARSAMRDLNT 156  
1758 ----FAHQKLEP-LTTTSQSGSHSTTIGAEFKKL-----SSQKSL----- 1797  
157 LQKKEELDIREFLEQMTLPDPSNCTIQNRDKNRYDILPDSYTRPLG-----KN 211  
1798 -----SSFASANLSCNKKRLNVLPTETTRVCLQPIRGVDG 1835  
212 KDYNASVIRVNHEBEYFYATQGPETIEDFWQVLENNCNVIAKITRECGVIKC 271  
1836 SDYNASPID--GYRYRAYIATQGPLDVEDFWALWESNCNIIIVMLTKLRMGREWC 1893  
272 YSYNPISLKEPLEHEHSVF-LETFHTVQFTVAVFOIVKSKGSCQVHKLFTKWPDH 330  
1894 HQYWP--SERARQYFVVDLAENWPQYI-LREFKVTARDGQSGTMRQFOLDNPEQ 1950  
331 GTPASADFFIKYRYVRKSH-----ITGPLLHCSAGVGRGTGVICVDVPSALEKNYSF 386  
1951 GVPSTGDFIDFIGQTHKTEKQFQCGQPIAVHCSAGVGRGTGVITLSIVLERNRFEAGVD 2010

QY 387 IMNIVTQMRKQRCGMIOTKEQYQCYEIVLEVL 419  
DB 2011 VFTQVNVLTQRPGMVQTEQYAFCYRAALEYL 2043  
RESULT 7  
Q9IA18 PRELIMINARY; PRT; 615 AA.  
AC Q9IA18;  
DT 01-OCT-2000 (TremBLrel. 15, Created)  
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)  
DE Receptor protein tyrosine phosphatase CRYP-alpha (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20193505; PubMed=10727868;  
RA Johnson K.G., Holt C.E.;  
RT "Expression of CRYP-alpha, LAR, PTP-delta, and PTP-zeta in the  
developing xenopus visual system";  
RL Mech. Dev. 92:291-294(2000).  
DR EMBL; AF138450; AAF43607.1; --  
DR HSP; F18052; IYFO.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR000242; Tyr\_PP.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SM00194; PTPC; 2.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE 1; 2.  
DR PROSITE; PS00056; TYR\_PHOSPHATASE 2; 2.  
DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
KW Hydrolase.  
FT NON TER.  
SQ SEQUENCE 615 AA; 70728 MW; 42593554887858AC CRC64;  
Query Match 22.2%; Score 496.5; DB 13; Length 615;  
Best Local Similarity 38.3%; Pred. No. 2.6e-30;  
Matches 110; Conservative 53; Mismatches 101; Indels 23; Gaps 8;  
QY 151 RDLNTLQKKEELDIREF--LEEQMTLPD-----ENSGNTLQNRDKNRYEDILPYD 202  
DB 326 RNLTYIQNLAQIDVGEHVIGMELEFRLANSKAHTSRFISANLPCNKFKNRLVINPYE 385  
QY 203 STRVPLG-----KNKDYINASYIRVNHEBEYFYATQGPETIEDFWQVLENNCNVI 257  
DB 386 TTRVCLQPIRGVSGSDYNASPID--GYRQCKAVIATQGPLAETTEDFWMLWENNSTIV 443  
QY 258 AMITREIECGVIKYSYWPISLKEPLEHEHSVF-LETFHTVQYFTVVRVQIVKSKGKS 316  
DB 444 VMLTKLRMGREKCHQWP--AERSARYQYFVVDMAEYNWPQYI-LREFKVTARDGQGS 500  
QY 317 QCVKELQTKWPDHGTFASADFFIKYRYVRKSH-----ITGPLLHCSAGVGRGTGVICV 372  
DB 501 RTVRQFQFTDWPQEGVPSKSGGFIDFIGQVHKTKEQSGDQGPISVHCSAGVGRGTGVITL 560  
QY 373 DWPSALEKNYSFIMNIVTQMRKQRCGMIOTKEQYQCYEIVLEVL 419  
DB 561 SIVLERMYEGVVDVDFQTVKRLQRTQRPANVQTEDEYQCYQAALLEYL 607  
RESULT 8  
Q9WU22 PRELIMINARY; PRT; 926 AA.  
AC Q9WU22;  
DT 01-NOV-1999 (TremBLrel. 12, Created)  
DT 01-NOV-1999 (TremBLrel. 12, Last sequence update)

T 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 E Testis-enriched protein tyrosine phosphatase.  
 N PTPN4.  
 S Mus musculus (Mouse).  
 C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 X NCBI\_TaxID=10090;  
 N [1]  
 P SEQUENCE FROM N.A.  
 C TISSUE=Testis;  
 K MEDLINE=20510023; PubMed=11054567;  
 A Park K.W., Lee E.J., Lee S.H., Lee J.E., Choi E.Y., Kim B.J.,  
 Hwang R., Park K.A., Baik J.H.;  
 I "Molecular cloning and characterization of a protein tyrosine  
 I phosphatase enriched in testis, a putative murine homologue of human  
 I PTPN4."  
 L Gene 257:45-55(2000).  
 C 1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.  
 R EXBL: AF106702; AAD22773.1; .  
 R HSP: P29350; IGW.  
 R MGD; MGI:1099792; Ptpn4.  
 R GO: GO:0004726; F:non-membrane spanning protein tyrosine phos. .; IDA.  
 R InterPro: IPR000239; Band 4.1.  
 R InterPro: IPR001478; PDZ.  
 R InterPro: IPR000387; TYR\_phosphatase.  
 R InterPro: IPR000242; Tyr\_PP.  
 R Pfam; PF00373; Band\_41; 1.  
 R Pfam; PF00395; PDZ; 1.  
 R Pfam; PF00102; Y\_phosphatase; 1.  
 R PRINTS; PR00935; BAND41.  
 R PRINTS; PR00700; PRTYPHPTASE.  
 R SMART; SM00295; B41; 1.  
 R SMART; SM00228; PDZ; 1.  
 R SMART; SM00194; PTEC; 1.  
 R PROSITE; PS00660; FERM\_1; 1.  
 R PROSITE; PS00661; FERM\_2; 1.  
 R PROSITE; PS0057; FERM\_3; 1.  
 R PROSITE; PS0106; PDZ; 1.  
 R PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 R PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 R PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 Q HYDROLASE.  
 W SEQUENCE. 926 AA; 105713 MW; A344DAD4FF7E2AE2 CRC64;  
  
 Query Match 22.1%; Score 495.5; DB 11; Length 926;  
 Best Local Similarity 27.5%; Pred. No. 5.5e-30;  
 Matches 136; Conservative 76; Mismatches 176; Indels 107; Gaps 12;  
  
 Y 2 SSPRKVRGKTR-----DNDEEGNSGN-LNLNS-----LPSSQKMTPTKP 43  
 b 450 SSPSPQETPDGQPPALPPKQSKNSWQIHPNSQQDLVTHNBSFDVPSPKSTPNGG 509  
 Y 44 IFGNKNSENVKPSHLSFSDKYELVYPPLESDDTETVMDVSDRLNRWNSMDSSETAG 103  
 b 510 IFDNLVLNKKKPDENGKRGFNGKGDQKMPVYSRVA-----PGT 551  
 Y 104 PSKTVSPVLSSGSRSLSKDTSTVSEKELTQIAQIRPLNPSGARSAMDCLNTLQKSEL 163  
 b 552 PADLCVPRLNQGVVQLNGRDIAERTHDQW----LFTKASCEKHSGLVLLVRNAVY 607  
 Y 164 DIIRFLELEF-----QMTLPDDFNNGNTI----- 187  
 b 608 DVVEEKLESPPDQYTEKAPLDSVQDDHLSRESMIQASGLITGVLAQPDQLYRKKP 667  
 Y 188 -----QNRDKRIRYDILPSTYPLGKNKYINASYIR-----IVNHEBYF 230  
 b 668 GMTWSCAKLPQNIQKRYRDISPYDATRVLLKGNEDYINANYINPEISSIIQ----- 722  
 Y 231 YIATQGLPPTIEDFQWLVNLCNVAMITREIECGVTKCYVYPISLKPLBEHEFSV 290  
 b 723 YIACQGLPPTCDPFWQMTVEQSSVMVMTTQVGRGVKCHQYWP-----EPSESSSYGC 778  
 Y 291 FLETFHVQ---YFTVRVFIKKSGKSCVKHLQFTKWPDRHGTGPASADFFIKYRVYR 347

Db 779 YQATCHSEGNPAYIFRKMVTLNKEKNSRQLTQIQTANPDHGVDDSSDFLDFVCHVR 838  
 QY 348 --KSHITGPELLVHCSAGVGRICGVFCVDWFSALKKYSFDDIMNIVTQMKQRCGMIOTK 405  
 Db 839 DQKAGKEPFIIVHCSAGIGRIGVLTMTMETCLIECQPVVPLDIVTRMDQRAMMIQTP 898  
 QY 406 EYQFCYEIVLEVLQ 420  
 Db 899 SQYRFVCEAILKVE 913  
  
 RESULT 9  
 Q9JULJ8 PRELIMINARY; PRT; 849 AA.  
 ID Q9JULJ8  
 AC Q9JULJ8;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE PTP35-B isoform.  
 GN PTPN4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DDY.  
 RK MEDLINE=20068798; PubMed=10600535;  
 RA Aoyama K., Maseuda T., Aoki N.;  
 RT "Characterization of newly identified four isoforms for a putative  
 RT cytosolic protein tyrosine phosphatase PTP36."  
 RL Biochem. Biophys. Res. Commun. 266:523-531(1999).  
 DR EXBL: AF170903; AAF27549.1; .  
 DR HSP; Q06124; 2SHP.  
 DR MGD; MGI:102467; Ptpn14.  
 DR GO: GO:0005856; C:cytoskeleton; IEA.  
 DR GO: GO:0016787; F:hydrolase activity; IEA.  
 DR GO: GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR000299; Band 4.1.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00373; Band\_41; 1.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PR00935; BAND41.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SM00295; B41; 1.  
 DR SMART; SM00194; PTEC; 1.  
 DR PROSITE; PS00660; FERM\_1; 1.  
 DR PROSITE; PS00661; FERM\_2; 1.  
 DR PROSITE; PS0057; FERM\_3; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Hydrolase. 849 AA; 97656 MW; 4945441F3F00B4EE CRC64;  
 SQ SEQUENCE. 849 AA; 97656 MW; 4945441F3F00B4EE CRC64;  
  
 Query Match 22.0%; Score 494; DB 11; Length 849;  
 Best Local Similarity 31.1%; Pred. No. 6.4e-30;  
 Matches 146; Conservative 72; Mismatches 156; Indels 96; Gaps 18;  
  
 QY 29 NSLPSSSQKMTPTKPIFGNK-----NSENKPSHLSFSDKYELVYPPLESDDTST 81  
 Db 395 NSL-SCSQSFQASPVSSNLSIPGSDIMRADYI-PSRHHS-----TIIVPSRPTPDYET 447  
 QY 82 VW-----DVSDRLNRWNSMDSSETAGSKTVSPVLSSGSRSLSKDTET----- 124  
 Db 448 VMEQMKRGLMHAADSQSKSLRN-LNIINHTAYNQPEL--VYSQPEKREHRYTPVPAHQG 504  
 QY 125 -----SVSEKELT-QLAQIRPLIF-----NNSARSAMEDCLNTLQK 159  
 Db 505 CYGHLNLEKQKMTGQKQKRPFLMLAALNGLSVARVSGREDGRHDATRPIDRLRALKK 564

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160 K3ELDIIRSELELEQNTLPDD-----FNSGNTLONRKNRYRDLPLVDSTVPL-----GK 210
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
565 KLEGDGV--FTYEQ--IENKQANGVFSTATLPENASREIREVPVPEENRVELIPTEN 620
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
211 NKDYINASIRIVNHEEEFYIATQGPLPETIEDFWOMVLNENCNVAMITRIEIGCVIK 270
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
621 NTGYINASHIKVVGSGEWHYIATQGPLPHTCHDFQWQVWQVGVNVLAVMTAEEGRTK 680
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
271 CVSYWPLSLKPLLEPHFSVPLETHVTQYF-----TVRFQIVKSTGSKQCVKHLQ 323
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
681 SHRYWP-----XLGSKHSATYKFKVTKTFTDSCGYATGLKVKHLLSQBSTVWHLQ 735
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
324 FTKWPDHGTSPASADFFIKY-----VRVVRKSHITG-----PLLVHCSAGVGTGVFTC 371
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
736 YTDWPHHGCPEDVQGFSLYLEBIQSVRRHTNSVLEGIRTRHPDPIVHCSAGVGTGVWL 795
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
372 VDVVPSAIEKNVSFDIMNIVTOMRKORCMIOITKEQYQPCHEIVLEVLQN 421
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
796 SELMIYCLEHNEKVEVPTMLRFREQRMFMIQTIAQKFKYQVLVQFLQN 845
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

SEQUIT 10
IBAO
Q9IBAO PRELIMINARY; PRT; 468 AA.
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
RYPTR2AC protein (Fragment).
RYPTR2AC.
Potamotrygon motoro (South American freshwater stingray).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalae; Hynosoelae; Prietorajea; Batorda;
Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.
NCBI_TaxId=86373;
[1]
SEQUENCE FROM N.A.
MEDLINE=20191325; PubMed=10754074;
Ono-Koyanagi K., Suga H., Katch K., Miyata T.;
"Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
divergence of tissue-specific isoform genes in the early evolution of
vertebrates.;"
J. Mol. Evol. 50:302-311(2000).
EMBL; AB033586; BAA95193.1; -.
HSSP; P18052; 1YFO.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:004725; P:protein tyrosine phosphatase activity; IEA.
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
InterPro; IPR000387; TYR_PP.
Pfam; PF00102; Y_phosphatase; 2.
PRINTS; PR00700; PRTVPHEPTASE.
SMART; SM00194; PTPC; 2.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
PROSITE; PS00506; TYR_PHOSPHATASE_2; 2.
PROSITE; PS00505; TYR_PHOSPHATASE_PTP; 2.
Hydrolase.
NON TER
SEQUENCE 468 AA; 53976 MW; 76C975D92D437A86 CRC64;

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Query Match      22.0%; Score 493.5; DB 13; Length 466;
Best Local Similarity 40.2%; Pred. No. 3.1e-30;
Matches 107; Conservative 48; Mismatches 90; Indels 21; Gaps 7;

170 LLEQMTLPD-----FNSGNTLQNRDKRYRDLPEYDSTRVPLG-----KKKDYINAS 218
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
200 MELEFKLANSKAHSTRISANLPCKNFKNLNMVEYETRVCLQPIRGVGSDYINAS 259
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

219 YRIVNHEEYPIATQPLPETTDFPMQWLENNCNVMIATREIEGVCYKCYSWNPIS 278
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

260 FID--GYRQKQAYIATQPLAETTFDFRMLENNNSTIVMLTKLRMGREKCHQYWP-- 315
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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QY	279	LKEPLEPHEHSVF-LETHVTVQYTVTRVFOIVKSGKSOCVKHLQFTKWPDHGTGPASAD	333
DB	316	AERSARYQYFVVDPMARYNMPQYI-LREFVTVTDARDQGSRTVRQFOFTDWPQGVKSGE	374
QY	338	PFIKVVRVVRKSH-----ITGPLLHVCAGAGRTGVFICVDVWVPSALEKNVSPDINNVITQ	393
DB	375	GRIDPIGVHKTQFGQDGPISVHCSAGAGRTGVITLSIVLERKRYEGVDIQTQVSK	434
QY	394	MKQRCGMIOKQYOQPCYEIVLEVL	419
DB	435	LRTQRPAMVQTEDEYQFCYQALEYL	460
RESULT 11			
Q90J34	PRELIMINARY;	PRT;	857 AA.
ID	Q90J34;		
AC	Q90J34;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Receptor protein-tyrosine phosphatase sigma (Fragment).		
DE	PTPRS OR RTPSIGMA.		
GN	Brachydanio rerio (Zebrafish) (Danio rerio).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinidae; Danio.		
OX	NCBI_TaxID=7955;		
OX	[1]_TaxID=7955;		
RP	SEQUENCE FROM N.A.		
RA	van der Sar A., Betist M., de Fockert J., Overvoorde J., Zivkovic D.,		
RA	den Hertog J.;		
RT	"Expression of receptor protein-tyrosine phosphatase alpha, sigma and		
RT	LAR during development of the zebrafish embryo.*"		
RL	Submitted (JUL-2603) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ311886; CAC44759.1; -.		
DR	ZFIN; ZDB-GENE-020107-3; Ptpns.		
DR	GO; GO:0016787; F:hydrolase activity; IEA.		
DR	GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.		
DR	GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.		
DR	InterPro; IPR008957; FN III-like.		
DR	InterPro; IPR000387; Tyr_P phosphatase.		
DR	InterPro; IPR000242; Tyr_Pp.		
DR	Pfam; PF00102; Y_phosphatase; 2.		
DR	PRINTS; PR00700; PTPYPTPTASE.		
DR	SMART; SM00194; PTPC; 2.		
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.		
DR	PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.		
DR	PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.		
FW	Hydrolase.		
KW	NON TER		
FT	SEQUENCE 857 AA; 97709 MW; 604A9226BB08B81D8 CRC64;		
QY	Query Match	22.0%; Score 493.5; DB 13; Length 857;	
DB	Best Local Similarity	38.1%; Pred. No. 7.1e-30;	
QY	Matches 110; Conservative	54; Mismatches 102; Indels 23; Gaps 8	
QY	149	AMRDCNLTLQKGBELDIRBF-LELEQMTLPD-----FNSGNTLNQRDKNRVRLP	200
DB	566	AARSLSFSYIQLAAGEHVSQMELEFKFLANSKAHTSRFISANLPCNKPKNRLVNP	625
QY	201	YDSTRVPLUG-----KNKDYINASVIRIVNHEBEFYIATQGPLTIEDFQMWLENNCN	255
DB	626	VETTRVCLQPIRGLEGGDYINSFID--GYRQKAVIATQGPLATTFDWRMLWENNST	683
QY	256	VIAMTIREICGVIKCYSWPISLKEPLBEHFSVP-LETFHTVQYTVTRVFOIVKSGTG	314
DB	684	IWMVLTKLREMGREKCHQWNP--AERSARYQYFVVDPMARYNMPQYI-LREFKVTDARDG	740
QY	315	KSOQVKHLQFTKWDHGTGPASADPFIKYRVVRKSH-----ITGPLLHVCAGAGRTGVFI	370
DB	741	GSRTVRQFOFTDWPQGVKSGGIDFGVQVHKTQFGQDGPISVHCSAGAGRTGVFI	800
QY	371	CVDVWVPSALEKNVSPDINNVITQVTRVFOIVKSGKSOCVKHLQFTKWPDHGTGPASAD	419



b 801 TLSIVLMRYEGVDFIQVTKMLRTQRPAMVQTEDEYQFCYQAALEYL 849

## RESULT 12

91BA2 Q91BA2 PRELIMINARY; PRT; 468 AA.  
 C Q91BA2;  
 T 01-OCT-2000 (Tremblrel. 15, Created)  
 T 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 T 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 E RyPTR22Ab protein (Fragment).  
 N RyPTR22AB.  
 S Potamotrygon motoro (South American freshwater stingray).  
 C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 C Elasmobranchii; Squalea; Hypnosqualea; Pristiogaster; Batoida;  
 C Myliobatiformes; Myliobatoidae; Potamotrygonidae; Potamotrygon.  
 X NCBI\_TaxID=86373;  
 X [1]  
 N SEQUENCE FROM N.A.  
 P MEDLINE=20219325; PubMed=10754074;  
 X Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;  
 A "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:  
 T divergence of tissue-specific isoform genes in the early evolution of  
 T vertebrates.";  
 T J. Mol. Evol. 50:302-311(2000).  
 L ENBL; AB033584; BAA95191.1; -.  
 R HSSP; P18052; IYFO.  
 R GO; GO:0016787; F:hydrolase activity; IEA.  
 R GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
 R GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 R InterPro: IPR000387; TYR phosphatase.  
 R InterPro: IPR000242; TYR\_PP.  
 R Pfam; PF00102; Y\_phosphatase; 2.  
 R PRINTS; PR00700; PRTYPHPTASE.  
 R SMART; SM00194; PTPC; 2.  
 R PROSITE; PS00383; TYR PHOSPHATASE 1; 2.  
 R PROSITE; PS00556; TYR PHOSPHATASE 2; 2.  
 R PROSITE; PS00555; TYR\_PHOSPHATASE\_PTP; 2.  
 R Hydrolase.  
 R NON TER  
 C SEQUENCE 468 AA; 5385 MW; 8B1CABE0BE962E4 CRC64;

Query Match 21.9%; Score 491.5; DB 13; Length 468;  
 Best Local Similarity 40.6%; Pred. No. 4.5e-30;  
 Matches 108; Conservative 46; Mismatches 91; Indels 21; Gaps 7;  
 Y 170 LELEQWTLDD-----FNSGNTLQNRDKRYRDLIPYDSTRVPLG-----KNKDYINAS 218  
 b 200 MELEFKRLANLKAHTSRFISANLPCNKKNLVIMPYESTRVCLQPIRGVSGSDYINAS 259  
 Y 219 YIRIVNHEEEFYIATQGLPETIEDFWQVLENNCNVMIATREIECGVIKCYSYWPIS 278  
 b 260 FID--GYRQKAYIATQGLAETTEDFWRLWENNSTIVVMTKLREMGREKCHQYWP-- 315  
 Y 279 LKEPLEFEHFSVP--LETHVTOYFTVRVQIVKSTGKSCQVXKHLQFTKPDHGTPTASAD 337  
 b 316 AERSARYQYFVVDPMAYENMPQYI--LREFKYTDARDGQSRVTRQFTDWPBQGVPSKSGE 374  
 Y 338 FFIKVRVYRKSH---ITGPLLHCSAGVGRGTGVFCVDVWFSALBKNSYFDMNIVTQ 393  
 b 375 GFIDFGVHKTKQFGQDGPISVHCSAGVGRGTGVFTLSIVLMRYEGVDFIQVTKM 434  
 Y 394 MKQRGCMIQTKQYQFCYVILEVL 419  
 b 435 LRTQRPAMVQTEDEYQFCYQAALEYL 460

## RESULT 13

Q9UM81  
 D Q9UM81 PRELIMINARY; PRT; 1502 AA.  
 C Q9UM81;  
 T 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE PTPSigma-(brain) precursor.  
 GN PTPSIGMA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 X [1]  
 N SEQUENCE FROM N.A.  
 P Endo N., Rutledge S.J., Opas E.E., Vogel R., Rodan G.A., Schmidt A.;  
 A "Human protein tyrosine phosphatase-sigma: Alternative splicing and  
 RT inhibition by biophosphonates.";  
 RL J. Bone Miner. Res. 0:0-0(1995).  
 DR ENBL; U41725; AAD09360.1; -.  
 DR HSSP; P18052; IYFO.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR003962; FNIII\_subd.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR008957; FN\_III-like.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003598; IG\_c2.  
 DR InterPro: IPR000387; TYR phosphatase.  
 DR InterPro: IPR000242; TYR\_PP.  
 DR Pfam; PF00041; fn3; 4.  
 DR Pfam; PF00047; IG; 3.  
 DR PRINTS; PR00102; Y\_phosphatase; 2.  
 DR PRINTS; PR00014; FNTYPEIIII.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SM00060; FN3; 4.  
 DR SMART; SM00408; IGc2; 2.  
 DR SMART; SM00194; PTPC; 2.  
 DR PROSITE; PS00835; IG LIKE; 3.  
 DR PROSITE; PS00383; TYR PHOSPHATASE 1; 2.  
 DR PROSITE; PS00556; TYR PHOSPHATASE 2; 2.  
 DR PROSITE; PS00555; TYR PHOSPHATASE\_PTP; 2.  
 K Hydrolase; Immunoglobulin domain; Signal.  
 FT SIGNAL 1 28 POTENTIAL.  
 SQ SEQUENCE 1502 AA; 168788 MW; AD6705AFEB0F3CFD CRC64;

Query Match 21.9%; Score 490.5; DB 4; Length 1502;  
 Best Local Similarity 40.2%; Pred. No. 2.6e-29;  
 Matches 107; Conservative 47; Mismatches 91; Indels 21; Gaps 7;  
 QY 170 LELEQWTLDD-----FNSGNTLQNRDKRYRDLIPYDSTRVPLG-----KNKDYINAS 218  
 Db 1234 MELEFKRLANLKAHTSRFISANLPCNKKNLVIMPYESTRVCLQPIRGVSGSDYINAS 1293  
 QY 219 YIRIVNHEEEFYIATQGLPETIEDFWQVLENNCNVMIATREIECGVIKCYSYWPIS 278  
 Db 1294 FID--GYRQKAYIATQGLAETTEDFWRLWENNSTIVVMTKLREMGREKCHQYWP-- 1349  
 QY 279 LKEPLEFEHFSVP--LETHVTOYFTVRVQIVKSTGKSCQVXKHLQFTKPDHGTPTASAD 337  
 Db 1350 AERSARYQYFVVDPMAYENMPQYI--LREFKYTDARDGQSRVTRQFTDWPBQGVPSKSGE 1408  
 QY 338 FFIKVRVYRKSH---ITGPLLHCSAGVGRGTGVFCVDVWFSALBKNSYFDMNIVTQ 393  
 Db 1409 GFIDFGVHKTKQFGQDGPISVHCSAGVGRGTGVFTLSIVLMRYEGVDFIQVTKM 1468  
 QY 394 MKQRGCMIQTKQYQFCYVILEVL 419  
 Db 1469 LRTQRPAMVQTEDEYQFCYQAALEYL 1494

## RESULT 14

Q90947  
 ID Q90947 PRELIMINARY; PRT; 832 AA.  
 AC Q90947;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)

RESULT 15	Q8RI69	PRELIMINARY;	PRT;	749 AA.
ID	Q8RI69			
AC	Q8RI69;			
DT	01-JUN-2002	(TrEMBLrel. 21, Created)		
DT	01-JUN-2002	(TrEMBLrel. 21, Last sequence update)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)		
DE	Hypothetical protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10909;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RA	Strausberg R.;			
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC025145; AAH25145.1; -;			
DR	PIR; S40282; S40282.			
DR	GO; GO:00046787; F:hydrolase activity; IEA.			
DR	GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.			
DR	GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.			
DR	InterPro; IPR000387; Tyr_phosphatase.			
DR	InterPro; IPR000242; Tyr_PP.			
DR	Pfam; PF00102; Y_phosphatase; 2.			
DR	PRINTS; PR00700; PTYRPHPTASE.			
DR	SMART; SM00194; PTPC; 2.			
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.			
DR	PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.			
DR	PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.			
KW	Hypothetical protein; Hydrolase.			
QY	SEQUENCE 749 AA; 86082 MW; 421FC6B9B50C959E CRC64;			
QY	Query Match	21.8%;	Score 489.5;	DB 11; Length 749;
Db	Best Local Similarity	40.2%;	Pred. No. 1.2e-29;	
Db	Matches 107; Conservative	46; Mismatches 92; Indels 21; Gaps 7;		
QY	170 LELQMTLPDD-----FNSGNTLQNRDKNRVDILPHYSTVPLG-----KKKDYINAS	218		
Db	481 MELFPRKLASKAHTSRFTSANTPCNKFNRLLVNMIPYESTVCLQPIRGVSGDYINAS	540		
QY	219 YIRIVNHEERYFIATQGPLPETIEDFWQWVLENNCNVIAMITRBTCCVIKCYSWPIS	278		
Db	541 PLD--GYRQKAVIATQGPLAEITDFWRLWEHNSTIVVMTKLREMGREKCHOYWP--	596		
QY	279 LKEPLEFEHSVP-LETFHTVQFTVVRVQIVKSTGSKSCQVKHLOFTKWPDHGCTPASAD	337		
Db	597 AERSARYQYFVDPMAEYNNPQI-LREFKVTARDQGSRTVRQCFDTPWBPQGVPKSGE	655		
QY	338 FFIKKVYVRKSH-----ITGFLAVHCSAGVGTGVFICVDVVFSAIEKNSYFDIMNIVTQ	393		
Db	656 GFDPFGQVHKTEQFGQDGFISVHCSAGVGTGVFITLSILERMRYEGVVDIFCTVKM	715		
QY	394 MKRQRCGMIOTKSQYOQFCYBEIVLEVL	419		
Db	716 LRTQRPAMVQTEQYQFCYRAALEYL	741		

4403 QTKBQYQFCYEIVLEV 419  
||:|||||:::|:  
4494 OTEEOYFIHDAIVEAI 510